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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 1, 2005, 18:05:25; Search time 109:109 Seconds (without alignments) 3214.888 Million cell updates/sec Run on:

US-09-591-632-2 3594 1 MSDSNQGNNQQNYQQYSQNG......FTLRDQGTTIAIGKIVKIAE 685

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched: 1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	1					-						Ol3354 candida alb	Q6q7i3 saccharomyc	Q6q7i6 saccharomyc		_	Q6q7i4 saccharomyc	Q6bwq4 debaryomyce	Q96uj2 saccharomyc	Q6q7il saccharomyc	Q96tj4 saccharomyc	Q96ui9 saccharomyc	Q96ujl saccharomyc	Q96uj0 saccharomyc	Q96ui8 saccharomyc	Q96tq9 saccharomyc		_		Q6cfc9 yarrowia li	Q7s6p5 neurospora
SUPERALES	ERF2_YEAST	Q9HGV1	QBTFB8	Q8TFR7	QSTFR8	Q6 FVM2	Q9HGI4	Q6CQF8	Q9HGI8	Q750T4	Q9HG17	ERF2_CANAL	Q6Q7 <u>T</u> 3	060716	Q6Q712	O9HGI6	Q6Q714	Q6BWQ4	Q96UJ2	060711	Q96TJ4	61096 <b>0</b>	Q96UJ1	Q96UJ0	Ø36UI8	Q96TQ9	Q96UJ3	ERF2_PICPI	Q9HGI5	Q6CFC9	Q7S6P5
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% Query Match Length	685	685	685	999	999	688	662	700	700	691	712	715	435	435	435	701	435	701	429	435	429	429	429	429	429	429	434	741	742	728	730
* Query Match	100.0	99.9	8.66	96.1	96.0		•	68.8	68.8	68.6	62.9	65.3	64.1	63.9	63.6	63.5	63.5	63.4	63.3	63.2	63.1	63.0	62.8	62.7	62.6	62.4	9.09	9.09	52.2	51.6	47.9
	3594	3590	3587	3455.5	3450.5	2632.5	2549.5	2471	2471	2464	2367	2345.5	2303	2296	2287	2283.5	2281	2277.5	2274	2272	2267	2263	2257	2253	2249	2243	2178	2177	1877	1855	1721
Result No.		2	co ·	4	ഗ	9	-	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

042787 podospora a		_	Q96gf2 homo sapien	Q91855 xenopus lae	_	Q6dd07 xenopus lae			Q9n2g7 oryctolagus		-	O88180 mus musculu	Q9ny44 homo sapien
042787	ERF2_SCHPO	Q96W <u>S</u> 7	Q96GF2	Q91855	Q7KZX8	Q6DD07	Q8K2E1	GSP1 HUMAN	Q9N2 <u>G</u> 7	Q6AYD5	QBCCV1	088180	Q9NY44
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716	662	629	633	614	498	553	587	499	588	636	498	597	628
47.7	47.0	45.2	38.3	38.3	38.0	37.8	37.8	37.7	37.7	37.7	37.6	37.5	37.5
1714	1689	1626	1377	1375	1364	1359.5	1357	1354.5	1353.5	1353.5	1352	1346.5	1346.5

## ALIGNMENTS

A CALLE	STANDARD; 420; (Rel. 09, Creat
22666	1. 09, Created)
1444	<ol> <li>09, Creat</li> </ol>
<b>5 5</b> 1	
<b>1</b>	01-NOV-1988 (Rel. 09, Last sequence update)
2	(REI. 43, nentide cha
88	
DE	н
S	Name=SUP35; Synonyms=GST1, PNM2, SAL3, SUF12, SUP2;
2 6	OrderedLocusNames=YDKI/ZW; OkrNames=YD4345.05;
20 0	Saccharomyces cerevisiae (baker's yeast). Dibarnota: Ringi: Ascomycota: Saccharomycotina: Saccharomycetes:
38	buvaiyota; rungi; secomytota; sactinaiomytotina; sactinaiomytota; Saccharomytetales: Saccharomytetateae: Saccharomytes.
ö	NCBI TaxID=4932;
RN	[1]
RP	
ž :	MEDILINESBESZYZ/Z/; PUDROGESZYZ/; PUDROGESZYZ/; PUDROGESZYZ/Z/; PUDROGESZYZ/Z/; PUDROGESZYZ/Z/; PUDROGESZYZ/Z/; PUDROGESZYZ/Z/; PUDROGESZYZ/Z/; PUDROGESZYZ/Z/; PUDROGESZYZ/Z/Z/Z/Z/Z/Z/Z/Z/Z/Z/Z/Z/Z/Z/Z/Z/Z/Z
5 2	
Z.	"Nucleotide sequence of the SUP2 (SUP35) qene of Saccharomyces
RT	
RL	Gene 66:45-54(1988).
RN	[2]
RP	
ž	bMed=3556215; DOI=10.1016/
<b>&amp;</b> ;	Kushnirov V.V., Ter-Avanesyan M.D., Surguchov A.P., Smirhov V.N.,
<b>8</b> 8	the second secon
1 E	Complete the control of the second of the se
¥ 5	Saccharomyces
2 :	, rett.
2 G	(5) SPOTIENCE FROM N A
A C	DECOLO 11
<b>1 2</b>	wilson P.G., Culbertson M.R.;
RT	"SUF12 suppressor protein of yeast. A fusion protein related to the
RT	-
Z.	VI.
Z :	
7 Y	SEQUENCE FROM NATIONAL SOLUTION
S S	impling-oggodit, functional A.; Kirkinchi V. Shimatake H. Kikuchi A.;
Ę Ł	t gene required for the G1
1 E	gene required for the or configuration concerns on A-kinase target site and GTPase domain.":
Z.	38).
RN	1
RP	SEQUENCE FROM N.A.
RC	STRAIN=S288C / AB972;
2	NE=97313263; PubMed=9169867;
≨ ;	Jacq C., Alt-Moerbe J., Andre B., Arhold W., Bahr A., Ballesta J.F.G.,
\$ 5	Bargues M., Barcon L., Becker A., Bireau N., Bloecker H., Blugeon C.,
<b>5</b> 5	BOSKOVIC J., BIGHAL F., BINGCAHEI M., BUILLAGO M.D., CORCEL F., Delaveau T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M.,

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RA Goffeau A., Gomez-Peris A., Granotier C., Hanemann V., Hankeln T.,
RA Kuester H., Laamanen P., Jimenez A., Jonniaux J.-L., Kraemer C.,
RA Kuester H., Laamanen P., Legros Y., Louis E.J., Moeller-Rieker S.,
Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,
RA Paulin L., Perea J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M.,
RA Rieger M., Salom D., Saluz H.P., Saiz J.E., Saren A.-M., Schaefer M.,
RA Scharfe M., Schmidt E.R., Schmeider C., Scholler P., Schwarz S.,
Urrestarazu L.A., Verhasselt P., Vissers S., Voet M., Volckert G.,
RA Wagner G., Wamburt R., Wedler E., Wedler H., Woelfl S., Chartles S.,
Hamlin N., Hunt S., Jones L., McDonald S., Murphy L., Niblett D.,
RA Malsh S.V. Barrell B.G. Dietrich F.S., Mulligan J.T., Allen E.,
Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M.,
RA Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A.,
Chung E., Duncan M., Hunicke-Smith S., Hyman R.W., Komp C.,
RA Definer P., Oh. C., Petel F.X., Roberts D., Schramm S., Schroeder M.,
Shogren T., Shroff N., Winant A., Yelton M.A., Botstein D.,
RA Hawkins J., Hillier L.W., Jier M., Johnson D., Johnston L.,
RA Hawkins J., Hillier L.W., Jier M., Johnson D., Johnston L.,
RA Hawkins J., Hillier L.W., Jier M., Johnson D., Johnston L.,
RA Hawkins J., Mandsh T., Langston Y., Latrellle P., Mardis E.,
Ritseten J., Ruebar T., Langston Y., Latrellle P., Wolldman P.,
Rales E., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman R.,
Raleine K., Mewes H.-W., Zollner A., Zaccaria P.,
Raleine K., Mewes H.-W., Zollner A., Zaccaria P.,
Rale Markerston R., Raterston R., Albermann K., Hani J., Hall
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Poznyakovski A.I., Paushkin S.V., Nierras C.R., Cox B.S.,
Ter-Avanesyan M.D., Tuite M.F.;
Ter-Avanesyan M.D., Tuite M.F.;
The products of the SUP45 (eRF!) and SUP35 genes interact to mediate translation termination in Saccharomyces cerevisiae.";
EMBO J. 144455-4373(1995).
The PUNCTION-TANOIVED IN Translation termination. Stimulates the activity of ERFI. Binds guanine nucleotides.
--- SUBUNIT: Heterodimer of two subunits, one of which binds GTP.
--- SUBCILILAR LOCATION: Cytoplasmic (Probable).
--- SIMILARITY: Belongs to the GTP-binding elongation factor family.
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                       TAREAR AND DESIGNATION OF THE COURT COURT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGI, SO00002539; SUP35.
GG); GO:0000288; P:mRNA catabolism, deadenylation-dependent; IMP.
InterPro; IPR004160; EFTU Cterm.
InterPro; IPR004161; EFTU _int _C.
InterPro; IPR009001; BIONG_init _C.
InterPro; IPR009000; ProtSyn_GTPbind.
InterPro; IPR009000; Translat_factor.
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PROSITE; PS00301; EPACTOR GTP; 1.
GTP-binding; Phosphorylation, Protein biosynthesis; Repeat.
DOMAIN
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Pfam; PF03144; GTP_BFTU D2; 1.
Pfam; PF03143; GTP_BFTU_D3; 1.
                                                                                                                                                                                                                                                                                                                                                                       EMBL; M21129; AAA35133.1; -.
EMBL; X07163; CAA30155.1; -.
EMBL; Y00829; CAA68760.1; -.
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ERF3 subfamily.
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                                                                                                                                                                                                                                                                                                                                              EPTKEPTKVEEPVKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAGROGWYLSWVMDTNKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGGAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETEN
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                                                                                                                                                                              1 MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERY
                                                                                                                                                      Gaps
         GTP (By similarity).

GTP (By similarity).

GTP (By similarity).

GTP (By similarity).

Interacts with GTP/GDP (By similarity).

Interacts with GTP/GDP (By similarity).

Phosphothreonine (By similarity).
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0
                                                                                                                            Length
                                                                                                                                                    Indels
                                                                                       S -> C (in Ref. 4).
43912A6D77DFA153 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                            100.0%; Score 3594; DB 1; 100.0%; Pred. No. 2.9e-175;
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                                                                                                                                                    0; Mismatches
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76551 MW;
                                                                                                                           Query Match
Best Local Similarity 100.'
Matches 685; Conservative
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  249
274
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685 AA;
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CONFLICT
SEQUENCE
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EQEEEVDDEVVNDMFGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYERAK 300
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Pfam; PF03144; GTP EFTU D2; 1.
Pfam; PF03144; GTP EFTU D2; 1.
PRINTS; PR0315; ELONGANTNFCT.
PRINTS; PR001343; YEASTERF.
PROSITE; PS00301; EPCOTOR GTP; UNKNOWN 1.
GTP-binding; Prion; Procein biosynthesis.
SEQUENCE 685 AA; 76609 MW; 43912A6DDBAF4E53 CRC64;
                                                                                                                                                          (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 3587; DB 2;
Pred. No. 6.6e-175;
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99.9%; Pred
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                                                                                                                                                                                                    Prion protein.
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05-JUL-2004
                                                                                                                                                                                                                 Name=SUP35;
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                            STRAIN-BSCTORY N.T.

A Resende C.G., Duarte J.B., Tuite M.F.;
Resende C.G., Duarte J.B., Tuite M.F.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

B Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005525; F:GTP binding; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

GO; GO:0006415; P:protein biosynthesis; IEA.

R InterPro; IPR004160; EFTU DC.

R InterPro; IPR004161; EFTU DZ.

R InterPro; IPR009001; Elong_init_C.

R InterPro; IPR009001; Elong_init_C.

R InterPro; IPR009000; Translat_factor.

R InterPro; IPR003285; Yeast_ERF.

R Pfam; PR00144; GTP_EFTU D2; 1.

R Pfam; PR0144; GTP_EFTU D2; 1.

R Pfam; PR0144; GTP_EFTU D2; 1.

R PRINTS; RR0135; ELONGATNFCT.

R PRINTS; RR0134; GTP_EFTU D3; 1.

R PRINTS; RR0134; FFACTOR GTP; UNKNOWN 1.
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99.9%; Pred. No. 4.6e-175;
tive 1; Mismatches 0;
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Matches 684; Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENTIALSCI2, and SCI6;

MEDINRE-277310; bubmed=12890024;

Resende C.G., Outerior T.F., Sands L., Lindquist S., Tuite M.F.;

The Prion protein gene polymorphisms in Saccharomyces cerevisiae.";

Mol. Microbiol. 49:1005-1017(2003).

Mol. Microbiol. 49:1005-1017(2003).

REMBL; AY028645; AAK26180.1; -.

SCD; S000002579; SUP35.

GO; GO:0003747; Fitzanalation release factor activity; IEA.

GO; GO:000341; Fitzanalational termination; IEA.

GO; GO:0006412; Fitzanalational termination; IEA.

RO; GO:0006412; Pitzanalational termination; IEA.

RO; GO:0006412; Pitzanalational termination; IEA.

RICEPPO; IPR004160; EFTU Cterm.

RICEPPO; IPR004161; EFTU Cterm.

RICEPPO; IPR004160; EFTU Cterm.

RICEPPO; IPR009101; BLOG init.C.

RICEPPO; IPR009000; Translat factor.

RICEPPO; IPR009000; Translat factor.

RICEPPO; IPR009000; Translat ERF. Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. ; Indels Length

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MEDLINE=22773310; PubMed=12890024;
Resende C.G., Outeiro T.F., Sands L., Lindquist S., Tuite M.F.;
"Prion protein gene polymorphisms in Saccharomyces cerevisiae.";
Mol. Microbiol. 49:1005-1017(2003).
MRBL; ARCS0846; PGTP binding; IEA.
GO; GO:0005525; FGTP binding; IEA.
GO; GO:0003747; F:translation release factor activity; IEA.
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
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                           QADVGVLVI SARKGEYETGFERGGOTREHALLAKTQGVNKMVVVVNKMDDPTVNMSKERY
                                                                                                                                                                                                                DOCUSINOSNELRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMN
                                                                                                                                                                                                                                                                                                                                                                                                                                               CVMHVHTAIBEVHIVKLLHKLEKGTNRKSKKPPAFAKKGMKVIAVLETEAPVCVETYQDY
                                                                                       QADVGVLV1SARKGEYETGFERGGOTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERY
                                                                                                                                                                         DOCVSNVSNPLRAIGYNIKTDVVPMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMN
                                                                                                                                                                                                                                                                   HVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETEN
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The prior protein gene polymorphisms in Saccharomyces cerevisiae.";

Mol. Microbiol. 49:1005-1017(2003).

EMBL; AX020847; AAK26178.1;

GO; GO:0005525; F:GTP binding; IEA.

GO; GO:0005412; F:grotein biosynthesis; IEA.

R GO; GO:0006412; F:grotein biosynthesis; IEA.

R GO; GO:0006412; F:grotein biosynthesis; IEA.

R GO; GO:0006412; F:grotein biosynthesis; IEA.

R GO; GO:0006415; F:translational termination; IEA.

InterPro; IPR004160; EFTU Cterm.

R InterPro; IPR004001; EDOM_init C.

InterPro; IPR009001; EDOM_init C.

InterPro; IPR009001; Translat factor.

R InterPro; IPR009001; Translat factor.

R InterPro; IPR009000; Translat factor.

R Pfam; PF03144; GTP_EFTU, D2; 1.

R Pfam; PF03144; GTP_EFTU, D2; 1.

R PRINTS; PR01315; ELOMGATERP.

R PROSTIE: PS00311; EFTU D2; 1.

R PROSTIE; PS00301; EFTU D2; 1.

R PROSTIE; PS00301; FFTU D2; 1.

R PROSTIE; PS00301; FTU D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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Pred. No. 3.2e-168;
0; Mismatches 1; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00301; EFACTOR GTP; UNKNOWN 1.
ng; Prion; Protein biosynthesis.
666 AA; 74408 MW; 13EA65612A0705F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               685
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MEDLINE-22773310; PubMed-12890024;
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01-JUN-2002 (TrEMBLrel. 21, La
01-MAR-2004 (TrEMBLrel. 26, La
Prion protein.
Name=SUP35;
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97.1%;
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Best Local Similarity 97.1
Matches 665; Conservative
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QUATER

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 666;
                 GO; GO: GOOGALIS; P: Translational termination; IEA.

InterPro; IPRO04160; EFTU Cterm.

InterPro; IPRO040161; EFTU D.2.

InterPro; IPRO04001; Elong init C.

InterPro; IPRO03009; ProtSyn GTPbind.

InterPro; IPRO03289; ProtSyn GTPbind.

InterPro; IPRO03289; ProtSyn GTPbind.

InterPro; IPRO03289; ProtSyn GTPbind.

InterPro; IPRO03289; ProtSyn GTP EFTU 1.

INTERPRO; IPRO03289; ProtSyn GTP EFTU D3; 1.

INTERPRO; PRO144; GTP EFTU D3; 1.

INTERPRO; PRO144; TP EFTU D4; 1.

INTERPRO; PRO144; TP EFTU D4; 1.

INTERPRO; PRO144; TP EFTU D3; 1.

INTERPROPER FOR TP TRANSPARE.

INTERPROPER FOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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Pred. No. 5.8e-168;
0; Mismatches 2;
GO:0006412; P:protein biosynthesis; IEA
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RESULT ( Q6FVM2 ID Q61

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-YONYO--GYSGYQQGGYQQYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYK 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boyers L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potter S., Richard G.F., Straub M.L., Suleau A.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Schlou-Meyer M., Zivanovic I., Bolctin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
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                                                                                                                                                                                   Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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R Mature 430:35-44(2004).

R GO; GO:0005525; F:GTP binding; IEA.

GO; GO:0006412; P:GTP binding; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

R GO; GO:0006412; P:protein biosynthesis; IEA.

R InterPro; IPR004161; EFTU Cterm.

R InterPro; IPR009001; Elong_init C.

R InterPro; IPR009001; Elong_init C.

R InterPro; IPR009001; Elong_init C.

R InterPro; IPR009001; ProteSyn GTPEind.

R InterPro; IPR009001; Iranslaf factor.

R Pfam; PF00144; GTP_ETTU; 1.

R Pfam; PF00144; GTP_ETTU D3; 1.

R Pfam; PF00143; GTP_ETTU D3; 1.

R PRINTS; PR00315; ELONGAÏNFCT.
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                          05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome E complete sequence.
Candida glabrata CBS138.
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SEQUENCE 688 AA; 77999 MW; 3BA760D47B74E3D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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74.2%; Pred. No. 3.2e-126;
ive 50; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00301; EFACTOR GTP; UNKNOWN 1.
Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome evolution in yeasts.";
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                                                                                                                                                                                                                                                    NCBI_TaxID=284593;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=CBS138;
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KKEEKKAEPKEQESKKEEP-KREGTPRPAAAKDEKKEDLPKLEKLKIKE---EQAAANAS 210
                                                                                                                                                                                                                                                         211 GADSLIKEQEEEVDEGVVNDMFGGKDHMSIIFMGHVDAGKSTWGGNILYMTGSVDKRTVE 270
                                                                                                                                                                                                                                                                                                               KYEREAKDAGKOGWYLSWVMDTNREERDDGKTIEVGRAYFETEKRRYTILDAPGHKMYVS 330
                                                                                                                 119 POSQGMSLNDFQKQQ---KQAAPKPKKTLKLVSSSGIKLANATKKVGTKPAESDKKEEEK 175
                                                                                                                                 YQQYNPDAGYQQQYNPQGGYQ-QYNPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAGFQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGGYQPYGGYQQFY--QDGQQAQQGAYNGYPYQ--AQGAPGGFN--NYNNQFQP-----Q
                                                                                                                                                                                                                                                                                                                                                                                                                               IYNETENEVDMAMCGEQVXLRIKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKS
                                                                                                                                                                                                                                   SADALIKEQEEEVDDEVVNDMFGGKDHVSLIFMGHVDACKSTMGGNLLYLTGSVDKRTIE
                                                                                                                                                                                                                                                                                              KYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVS
                                                                                                                                                                                                                                                                                                                                                                      EYLDTMNHVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I I AAGFSCVMHVHTA I BEVH I VKLLHKLEKGTNRKSKKPPAFAKKGMKVI AVLETEAPVC
MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGY-QAYNAQAQPAGGYYQNYQGYSGYQQGG
                       -----QGGQQNAGGNYYQQYFQKLTQQAQ-AGGGYQPYGGYGGY--GG
                                                                                                                                                                          SAETK--EPTKEPTKVEEPVKKEEKPVOTEEKTEEKSELPKVEDLKISESTHNTNNANVT
                                                                                                                                                                                                                                                                                                                                                         EMIGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTV
                                                                                                                                                                                                                                                                                                                                                                                                                  NWSKERYDQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kluyveromyces lactis NRRL Y-1140.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI_TaxID=284590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
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ORFNames=KLLA0D17424g;
                          MSDPNO-NGO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=NRRL Y-1140;
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                                                                                                                   AKTQGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21324710; PubMed=11430816; DOI=10.1016/S1097-2765(01)00259-3; Nakayashiki T., Ebihara K., Bannai H., Nakamura Y.; "Yeast (PSI+] 'prions' that are crosstransmissible and susceptible beyond a species barrier through a quasi-prion state."; Mol. Cell 7:1121-1130(2001). EMBL; AB039753; BAB12684.2; -GO; GO:0005525; F:GTP binding; IEA. GO; GO:0003747; F:translation release factor activity; IEA. GO; GO:0006412; P:protein biosynthesis; IEA. GO; GO:0006412; P:protein biosynthesis; IEA.
 KSTMGGNLLYLTGSVDKRT1EKYEREAKDAGRQGWYLSWVMDTNKEERNDGKT1EVGKAY
                  KSTWGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIEVGKAY
                                                                         FETEKRRYTILDAPGHKMYVSEMIGGASQADVGILVISARKGEYETGFEKGGQTREHALL
                                                                                                                                  KNPIKNVTRFVAQIAIVELKSIMSAGFSCVMHVHTAIBEVHITRLLHKLERGTNRKSKKP
                                                          FETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTREHALL
                                                                                                                                                                              ANLKDHVDPKECPWYTGPTLLEYLDTWNHVDRHINAPFMLPIAAKWKDLGTIVEGKIESG
                                                                                                                                                                                                                                        HIKKGOSTLLMPNKTAVEIQNIYNETENEVDMAMCGEQVKLRIKGVEBEDISPGFVLTSP
                                                                                                                                                                                                                                                                                                KNPIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                            685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zygosaccharomyces rouxii (Candida mogii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.
NCBI_TaxID=4956;
                                                                                                                                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.9%; Score 2549.5; DB 2; Length 662; Best Local Similarity 74.0%; Pred. No. 5.2e-122; Matches 512; Conservative 53; Mismatches 90; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73780 MW; 2641046199FB1E04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-UIN-2001 (TrEMBLrel. 17, Last sequence update)
01-UAR-2004 (TrEMBLrel. 26, Last annotation update)
Polypeptide release factor 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 662
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InterPro; IPR004161; EFTU Cterm.
InterPro; IPR0040161; EFTU Cterm.
InterPro; IPR0009001; EDONG_init_C.
InterPro; IPR0009001; Translat_factor.
InterPro; IPR0090000; Translat_factor.
InterPro; IPR0030805; Yeast_ERF.
Pfam; PF00109; GTP_EFTU D2; 1.
Pfam; PF01314; GTP_EFTU D2; 1.
PRINTS; PR01313; YEASTERF.
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GTP-binding,
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Q9HG14;
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111 ÇGYĞGAQGYNAQQPTGYAAPAQSSSĞGMTLKDFQNQQGSTNAAKPKPKLKLASSSGIKLV 170
                                       PIAAKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAMCGEQVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AB039749; BAB12680.1; -. 600.0005525; F.GTP binding; IEA. GO; GO:0005525; F.GTP binding; IEA. GO; GO:0003747; F.translation release factor activity; IEA. GO; GO:0006412; P:protein biosynthesis; IEA. GO; GO:0006415; P:translational termination; IEA. InterPro; IPR004160; EFTU Cterm.
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PEAM; PP00109; GTP EFTU; 1.
PEAM; PP03144; GTP EFTU D3; 1.
PRINTS; PR00315; ELONGATNECT.
PRINTS; PR00316; EASTERF.
PROSITE; PS00301; EFACTOR GTP; UNKNOWN 1.
GTP-binding; Protein biosynthesis.
SEQUENCE 700 AA; 77638 MW; 53F9905442F6B025 CRC64;
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Last sequence update)
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68.2%; Pred. No. 5.6e-118;
ive 56; Mismatches 95;
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InterPro; IPR000709; ProtSyn GTPbind.
InterPro; IPR009009; Translat factor.
InterPro; IPR003285; Yeast_ERF.
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01-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2004 (TrEMBLrel. 26, L
Polypeptide release factor 3.
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Local S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 QGYQGAQGYNAQQPTGYAAPAQSSSQGMTLKDFQNQQGSTNAAKPKPKLKLASSSGIKLV 170
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Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerteet A., Koszul R., Lemairem M., Lesur I., Ma L., Muller H., Nikolski R., Lemairem M., Lesur I., Ma L., Muller H., Nikolski R., Strand J.M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Westolowski-Louvel M., Westhoff E., Wirth B., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wicker P., Soudiet J.L.,
"Genome evolution in yeasts.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0006412; F:translation release factor activity; IEA.
GO; GO:0006415; P:translational termination; IEA.
R GO; GO:0006415; P:translational termination; IEA.
R InterPro; IPR004160; EFTU Cterm.
R InterPro; IPR004161; EFTU D2.
R InterPro; IPR00901; Elong_init C.
InterPro; IPR00915; ProtSyn GTPbind.
R InterPro; IPR00915; ProtSyn GTPbind.
R Pfam; PF00144; GTP_EFTU 1.
R Pfam; PF00143; GTP_EFTU 1.
R Pfam; PF00143; GTP_EFTU 1.
R Pfam; PF0143; GTP_EFTU 1.
R Pfam; FF0143; GTP_EFTU 1.
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00 AA; 77638 MW; 53F9905442F6B025 CRC64;
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Matches 500; Conservative
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
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MEDIANE\_213-2470; PubMed=11430816; DOI=10.1016/S1097-2765(01)00259-3;
MEDIANE\_213-24700; PubMed=11430816; DOI=10.1016/S1097-2765(01)00259-3;
MARAYASHIKI T., Ebihara K., Bannai H., Nakamura Y.;
"Yeast [PSI+] 'prions' that are crosstransmissible and susceptible beyond a species barrier through a quasi-prion state.";
MOI Cell 7:1121-1130(S00.1; -.. Kluyverčnyćes lactis (Yeast). Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces. 82;

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                                                                                                                                                                                                                                                                                                                                    QQGGYQQYNP-DAGYQQQYNPQGGYQQYNPQGGYQ--QQFN--PQGGRGNYKNFNYNNUL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPNKTAVELQNIYNETENEVDWAMCGEQVKLRIKGVEEEDISPGFVLTSPKNPIKSVTKF 582
                                                                                                                                                                                                                                                                                                                                                                                                                      QGYQAGFQPQSQGMSLNDFQK--QQKQAAPKPKKTLKLVSSSGIKLANATKKVGTKPAES 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPK 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                             169 DKKEBEKSAETKEPTKEPTK--VEEPVKKEEKPVQTEEKTEEKSELPKVEDLKISES---
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                                                                                                                                                                                                                                                                                      NQGQGQQNFGQYYNPSNFQ----NYQGYVPQGGYQAYGQQAGGYQGYAQYNQQAGGYQGY
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                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Polypeptide release factor 3.
Name=sup35;
Candida maltosa (Yeast).
Bukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TAXID=5479;
                                                                                                                                                                                                 58;
                                                                                                                                                   68.6%; Score 2464; DB 2; Length 691; 71.1%; Pred. No. 1.3e-117; ive 52; Mismatches 93; Indels 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAVLETEAPVCVETYQDYPQLGRFTLRDQGTTIAIGKIVKIAE 685
                                                                                                         76193 MW; 8B38099C60EB9509 CRC64;
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Last sequence update)
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                PRINTS; PR00315; ELONGATNECT.
PRINTS; PR01343; YEASTERF.
PROSITE; PS00301; EFACTOR GTP; UNKNOWN 1.
GTP-binding; Protein biosynthesis.
PF03144; GTP EFTU D2; 1
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(TrEMBLrel. 17, I
(TrEMBLrel. 26, I
                                                                                                                                                   Query Match 68.6%;
Best Local Similarity 71.1%;
Matches 500; Conservative 5
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DDLKISEAEKPKTKENTPSADDTSSEKTTSAKADTSTGGANSVDALIKEQEDEVDEEVVK 266
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                                                                                                                                                                                                     DMFGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWV 312
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                                                                                                                                                                                                                            DMFGGKDHVSIIFMGHVDAGKSTMGGNLLYLTGSVDKRTVEKYEREAKEAGROGWYLSWV
                         NATKKVGTKPAESDKKEEEKSAETKEPTKEPTKVEEPVKKEEKPVQTEEKTEEKSELPKV
                                                                                                                EDLKISE-----STHNTNNANVTSA------DALIKEQEEEVDDEVVN
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
AGL145Wp.
ORFNames=AGL145W;
Ashbya gossypii (Yeast) (Eremothecium gossypii).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetales; Combine (International Combine (Internatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
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Lerch A., Brachat S., Voegeli S.E., Gaffney T., Philippsen Dietrich F.S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AE016820; AAS54346.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor activity;
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GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0005412; P:protein biosynthesis; IEA.
GO; GO:0006415; P:translational termination; IEA.
InterPro; IPR004161; EFTU D2.
InterPro; IPR000001; Elong_init C.
InterPro; IPR000001; Promainity C.
InterPro; IPR000000; Translat factor.
InterPro; IPR001285; Protest ERF.
PFGm; PF00009; GTP_EFTU; I
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                                                                  GAKKPVAPK-----TEKTDESKEATK----
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1 MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQ----PAGGY--YQNYQGYSG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity of ERF1. Binds guanine nucleotides.
SUNCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the GTP-binding elongation factor family.
ERF3 subfamily.
                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Eukaryotic peptide chain release factor GTP-binding subunit (ERF2)
(Translation release factor 3) (ERF3) (ERF-3).
                                                             KSKKPPAFAKKGMKVIAVLETBAPVCVETYQDYPQLGRFTLRDQGTTIAIGKIVKI
                                                                                                                                                                                                                                                                                                                                                                                                                    "The Candida albicans Sup35p protein (CaSup35p): function, prion-behaviour and an associated polyglutamine length polymorphism."; Microbiology 148:1049-106(02002); Profession termination. Stimulates the -FUNCTION: Involved in translation termination.
                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity)
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PRINTS; PR00315; ELONGATNFCT.
PROSTTE; PS00301; EFATTOR GTP; 1.
GTP-binding; Phosphorylation; Protein biosynthesis; Re
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GTP (By similarity).
GTP (By similarity).
GTP (By similarity).
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rive 77; Mismatches 120;
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InterPro; IPR004160; EFTU Cterm.
InterPro; IPR004160; EFTU CT.
InterPro; IPR009001; Elong init C.
InterPro; IPR000195; ProtSyn GTPbind.
InterPro; IPR000000; Translat_factor.
Pfam; PF000009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU D2; 1.
Pfam; PF03144; GTP_EFTU D2; 1.
                                                                                                                                                                                                                                                                                                                                                            STRAIN=2005E;
MEDLINE=21930287; Pubmed=11932450;
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                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
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                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                      Name=SUP35;
Candida albicans (Yeast)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----PSV-----ASKSAPVSASASVVTADALAKEQEDEVDEEVVKDMFGGKDHVSIIFMG
                           HVDAGKSTWGGNILYLTGSVDKRTVEKYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNQGNNQQNYQQYSQ-NGNQQQGNNRYQGYQAYNAQAQPA-GGYYQNYQGYSGYQQGGYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 QQQQQQTQSQGMSLADFQKQKAEQQASLNKPAVKKTLKLASSSGIKLANATKKVDTAKPA
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 712;
                                                                                                                              GO:0005525; F:GTP binding; IEA.
GO:0003747; F:translation release factor activity; IEA
GO:0006412; P:protein biosynthesis; IEA.
GO:0006415; P:translational termination; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                         78631 MW; 729B6A814735C469 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    65.9%; Score 2367; DB 2; 67.7%; Pred. No. 1.2e-112; ive 61; Mismatches 108;
                                                                                                                                                                                       InterPro; IPR004160; EFTU Ctern.
InterPro; IPR004161; EFTU D2.
InterPro; IPR009011; Elrqu d_init_C.
InterPro; IPR009010; Elrqu d_init_C.
InterPro; IPR009000; Translat_factor.
InterPro; IPR003085; Yeast_ERF.
InterPro; IPR003085; Yeast_ERF.
Pfam; PF00144; GTP_EFTU; D1.
Pfam; PF03143; GTP_EFTU D2; 1.
PRINTS; PR01343; GTP_EFTU D2; 1.
PRINTS; PR01343; YEASTERF.
PROSITE; P801301; EFACTOR_GTP; UNKNOWN 1.
GTP-binding; Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 485; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        712 AA;
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GYQQQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAGFQPQSQGMSLN 127
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                                                                                                                                                                                                                                                                                   KVEEPVKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKEQEBEVD
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                                                                                                                                                                                                                                                                 NNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDA
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NCBI_TaxID=4932;
                          activity; IEA
                                                                                                                                                                                                           Length
                                                                                                                                                                               48968 MW; ED0E85699BB28442 CRC64;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Translation termination factor SUP35 (Fragment).
Name=SUP35;
                                                                                                                                                                                                          64.1%; Score 2303; DB 2; 1
100.0%; Pred. No. 1.1e-109;
     GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0005425; F:GTP binding; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
GO; GO:0006415; P:protein biosynthesis; IEA.
InterPro; IPR003795; ProtSyn_GTPbind.
InterPro; IPR003785; Veast ERF.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; UNKNOWN_1.
GTP-binding; Protein biosynthesis.
NON_TER 1 1
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Matches 435; Conservative 0; Mismatches
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AAS64326.1;
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                                                                                                                                                                                 435 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHI 614
                                                                                                                            KVGT--KP-----TKEPTKVEEPVK 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAKWKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAMCGEQVKLR 554
              YQQ-GGYQQYNP-DAGYQQQYNPQGGYQQ-YNPQGGYQQQFNPQGGRGNYKNFNYNNNLQ 111
                                                                                                                                                                                               FGGKDHVSIIFMGHVDAGKSTMGGNILYLTGSVDKRTVEKYEREAKDAGRQGWYLSWVMD
                                                                                                                                           FGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMD
                                                                    GYQA-GFQP-----QSQGMSLNDFQKQ--QKQAA---PKPKKTLKLVSSSGIKLANATK
                                                                                                                                                                                  KEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKEQEEEVDDEVVNDM
                                                                                                                                                                                                                                                                                                TNKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKG
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"Population genetic variation in gene expression is associated with phenotypic variation in Saccharomyces cerevisiae.";
Genome Biol. 5:R26-R26(2004).
EMBL, AYS53987; AAS643281; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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Translation termination factor SUP35 (Fragment)
Name=SUP35;
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PubMed=15059259;
Pay J.C., McCullough H.L., Sniegowski P.D., Eisen M.B.;
Population genetic variation in gene expression is associated with phenotypic variation in Saccharomyces cerevisiae.";
Genome Biol. 5:R26-R26 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                   GO, GO:0005525; F:GTP binding; IEA.
GO, GO:000525; F:GTP binding; IEA.
GO, GO:0003747; F:translation release factor activity; IEA.
GO, GO:0006412; P:protein biosynthesis; IEA.
GO, GO:0006412; P:translational termination; IEA.
InterPro; IPR000795; ProtSyn GTPbind.
InterPro; IPR003285; Yeast ERF.
PRINTS; PR00315; ELONGATNFGT.
PRINTS; PR01313; YEASTERF.
PROSITE; PS00301; EFACTOR GTP; UNKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                               63.9%; Score 2296; DB 2; 99.8%; Pred. No. 2.6e-109;
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05-JUL-2004 (TrEMBLrel. 27, Last seq
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  AY553984; AAS64325.1;
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Matches 434; Conservative
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DR GO; GO:0005525; F:GTP binding; IEA.

GO; GO:0005525; F:GTP binding; IEA.

DR GO; GO:000347; F:translation release factor activity; IEA.

GO; GO:0006415; P:translational termination; IEA.

BR GO; GO:0006415; P:translational termination; IEA.

InterPro; IPR000795; ProtSyn GTPbind.

R InterPro; IPR0013285; Yeast ERF.

R RINTS; PR01343; YEASTERF.

R PRINTS; PR01343; YEASTERF.

R PROSITE; PS00310; EPACTOR GTP; UNRNOWN 1.

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Pred. No. 7.5e-109;
1; Mismatches 2;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 1, 2005, 18:05:05; Search time 191.103 Seconds (without alignments) 1386.327 Million cell updates/sec

US-09-591-632-2

1 MSDSNQGNNQQNYQQYSQNG.....FTLRDQGTTIAIGKIVKIAE 685 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched: Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp1990s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003s:\* geneseqp2003bs:\* geneseqp2003bs:\* A\_Geneseq\_16Dec04:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Aab30792 Amino aci	Abr53107 Protein s	Adk63022 Disease t	Abp73437 Candida a	Aab30820 Amino aci	Aab30819 Amino aci	Ads44300 Bacterial	Adb70240 C. neofor	Ab 326050	Abj25450 Aspergill		Adc35080 Human bre	Adn03793 Antipsori	Adp54304 Human PRO	Adp24765 PRO polyp	_	Adn99777 Novel hum	Aab92825 Human pro	Aab30800 A modifie	Abb62309 Drosophil	Aaw37508 Human GSP	Abr56523 Human GSP	Adq76519 Amino aci		Aab30799 A modifie
	AAB30792	ABR53107	ADK63022	ABP73437	AAB30820	AAB30819	ADS44300	ADB70240	ABJ26050	ABJ25450	ADM04489	ADC35080	ADN03793	ADP54304	ADP24765	ADR99225	ADN99777	AAB92825	AAB30800	ABB62309	AAW37508	ABR56523	ADQ76519	AAB94470	AAB30799
в 1D	4 AAB	5 ABR	7 ADK	5 ABP	4 AAB	4 AAB	B ADS	7 ADB	6 ABJ	6 ABJ	7 ADM	7 ADC	3 ADN			8 ADR		4 AAB	4 AAB	Ī	2 AAW		8 ADQ	4 AAB	4 AAB
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## ALIGNMENTS

Sup35; phenotype; SCHAG; self-coalesce; higher-order aggregate; amyloidogenic domain; aggregation; fibril; phenotypic alteration; gene therapy; disease resistance; plant pigmentation; prion disease. Amino acid sequence of a yeast Sup35 protein. AAB30792 standard; protein; 685 AA. 02-APR-2001 (first entry) Saccharomyces cerevisiae. AAB30792; AAB30792 

WO200075324-A2

14-DEC-2000.

09-JUN-2000; 2000WO-US015876.

99US-0138833P. 09-JUN-1999;

(ARCH-) ARCH DEV CORP.

Liu J, Sondheimer N, Scheibel T; <sup>ر</sup>ا Ψa Li L, Lindquist S,

WPI; 2001-061723/07. N-PSDB; AAC86679. New nucleic acid encoding chimeric proteins with self-assembly properties, useful e.g. for diagnosis and treatment of prion diseases, also related aggregates, fibrils and polymers.

Claim 11; Page 125-127; 188pp; English.

The present sequence represents a yeast Sup35 protein. The protein possesses the prion-like capacity to undergo a self-perpetuating conformational alteration that changes the functional state of Sup35 in a manner that creates a heritable change in phenotype. It is used to construct chimeric polypeptides of the invention, which comprise at least one SCHAG (self-coalesces into higher-order aggregates) amino acid sequence fused in frame with a polypeptide of interest (which is other than a marker protein, a glutathione-S-transferase or a staphylococcal nuclear protein). The specification also describes chimeric polypeptides that comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with

20-DEC-2001; 2001EP-00130253 15-MAY-2001; 2001EP-00111774

20-NOV-2002

cerevisiae

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 or specific binding
multiple reactivities, e.g. derivatised with enzymes, or specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used create an inducible, or stable phenotypic alteration in a cell, e.g. for gene therapy, protein production, imparting disease resistance to plants, altering plant pigmentation and for diagnosis and treatment of prion diseases
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100.0%; Pred. No. 2.9e-241;
tive 0; Mismatches 0;
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The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or discorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or discorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete
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Superti-Furga GD;
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Best Local Similarity 100.
Matches 685; Conservative
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M, Schultz JD,
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N-PSDB; ACC61149.
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Marzioch
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Multiprotein complex; eukaryote; drug target; diagnosis.

Protein sequence #SEQ ID 1079

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                                                              HVDRHINAPFWLPIAAKWKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETEN
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           DQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMN
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Kruse U, Merino A, Bauch
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P, Krause R, F
IC, Rick J;
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Michon A, Leutwein C,
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M, Grandi
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data for
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                                                                                                                                                                                                                                                                                                                                                        SQGMSLNDFQKQQKQAAPKPKKTLKLVSSSGIKLANATKKVGTKPAESDKKEEEKSAETK
                                                                                                                                                                                                                                                                                                                                                                          EQEEEVDDEVVNDMFGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYERAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 EQEEEVDDEVVNDMFGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 EVDWAMCGEQVKLRIKGVBEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAGFQPQ
                                                                                                                                                                                                                                                                                                                                                                                                                               EPTKEPTKVEEPVKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 QADVGVLVISARKGEYETGFERGGOTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOCVSNVSNFLRAIGYNI KTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HVDRHINAPFMLPIAAKWKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVDMAMCGEQVKLRIKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKPPAFAKKGMKVIAVLETEAPVCVETYQDY
                                                                                                                                                                                                        1 MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGY
                                                                                                                                                                                                                                          1 MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERY
                                                                                                                                                                     Gaps
for the treatment or prevention of a disease or disorder. This sequencesponds to a protein of the invention. (Note: the sequence date this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal.
                                                                                                                                                                   ö
                                                                                                                                 Length
                                                                                                                                                                   Indels
                                                                                                                               100.0%; Score 3594; DB 7;
100.0%; Pred. No. 2.9e-241;
tive 0; Mismatches 0;
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                                                                                                                                                  Best Local Similarity 100.
Matches 685; Conservative
                                                                                                 Sequence 685 AA;
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Best Local 9
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-AKDDIIYMPVSGYTGAGLKDRVDPKDCPWYDGPSLLEYLDNMDTMNRKINGPFMMPVSG 533
              EKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKEQEEEVDDEVVNDMFG 256
                                                                                                                                                                                                                                                                NIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMNHVDRHINAPFMLPIAA 496
                              ATPTPAAKK--ESTPTPATATKK--ESTPVSNSASVATADALVKEQEDEIDEEVVKDMFG
                                                                                            GKDHVSIIFMGHVDAGKSTWGGNILYLTGSVDKRTVEKYEREAKDAGKQGWYLSWWDTN
                                                                                                                                                          KEERNDGKTIEVGKAYFETDKRRYTILDAPGHKMYVSEMIGGASQADVGILVISARKGEY
                                                                         GKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTN
                                                                                                                                       KEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEY
                                                                                                                                                                                                  ETGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGY
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IGKITKL 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida albicans.
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                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by the promoter replacement fragment with a heterologous promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that cells having both alleles modified are useful for identifying a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential Candida albicans protein used in the method of the invention.

Note: The sequence data for this patent is not represented in the printed of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 PQQQQQYGGYNQYNQYQGGYQQNYNNRGGYQQSYNNRGGYQQNYN---NRGGYQGYNQN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQYGGYQQYNSQPQQQQQQQQGMSLADFQKQKTEQQASLNKPAVKKTLKLAGSSGIKLA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATKKVGT--KP-------AESDKKEEERKSAETKEPTKEPTKPTKF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GYSGYQQ-GGYQQYNP-DAGYQQQYNPQGGYQQ-YNPQGGYQQQFNPQGGRGNYKNFNYN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 NNLQGYQA-GFQP-----QSQGMSLNDFQXQ--QKQAA---PKPKKTLKLVSSSGIKLA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification but is based on sequence information supplied to Derwent by
the European Patent Office
                                                                                                                                                                                                                                                                                                                Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 NNQQNYQQY-----BQNGN---QQQGNNRYQGYQAYNAQAQ----PAGGY--YQNYQ 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDOONTODOLSGAMANASLNGDQSKOOOOOOOOOONYYNPNAAQSFVPQGGYQQFQQFQ 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
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                                                                                                                                                                                                                                                                                                                                                                              Claim 44; SEQ ID NO 7274; 167pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.3%; Score 2347.5; DB 5; Length 64.8%; Pred. No. 1.6e-154; ive 79; Mismatches 118; Indels
                                                                                                                                                                                                                                    Ohlsen KL;
                                                                                                                                                                                                                                    Bussey H,
                                                                                                                                                                                                                                    Boone C,
                                                                                                                                     29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                         26-DEC-2001; 2001WO-US049486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 471; Conservative
                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                    Jiang B,
                                                                                                                                                                                                                                                                   2002-566694/60.
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                Candida albicans
                                                                                                                                                                                                                                                                                   N-PSDB; ABZ31987
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                                            WO200253728-A2
                                                                                                                                                                                                                                    Roemer T,
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KMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAMCGEQVKLRIK 556
                               GVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHIVK 616
                                                                                                                                              617 LLHKLEKGTNRKSKKPPAFAKKGMKVIAVLETEAPVCVETYQDYPQLGRFTLRDQGTTIA 676
                                                                                                                                                                                                                                                                           New nucleic acid encoding chimeric proteins with self-assembly
properties, useful e.g. for diagnosis and treatment of prion diseases,
also related aggregates, fibrils and polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHAG; self-coalesce; higher-order aggregate; amyloidogenic domain; aggregation; fibril; phenotypic alteration; gene therapy; disease resistance; plant pigmentation; prion disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of a Candia albicans protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 175-177; 188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB30820 standard; protein; 715 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39-JUN-2000; 2000WO-US015876.
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AAB30819

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one SCHAG (self-coalesces into higher-order aggregates) amino acid sequence fused in frame with a polypeptide of interest (which is other than a marker protein, a glutathione-S-transferase or a staphylococcal nuclear protein). The specification also describes chimeric polypeptides that comprises an amyloidogenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with multiple reactivities, e.g. derivatises are used to prepare polymers with partners, and useful e.g. for performing multi-step chemical reactions. They can be used create an inducible, or stable phenotypic alteration in a cell, e.g. for gene therapy, protein production, imparting disease resistance to plants, altering plant pigmentation and for diagnosis and treatment of prion diseases. The present sequence is used in the course
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQQYGGYNQYNQYQGGYQQNYNNRGGYQQGYNNRGGYQQNYN---NRGGYQGYNQNQQYG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYQA-GFQP-----QSQGMSLNDFQKQ--QKQAA---PKPKKTLKLVSSSGIKLANATK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AESDKKEEEKSAETKEP----TKEPTKPFPVK 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQ----PAGGY--YQNYQGYSG
                                                                                                                                                                                                                                                                                                                                                                                                                          KEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKEQEEEVDDEVVNDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMD
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                                                                                                                                                                                                                                                                                                                                                      61;
                                                                                                                                                                                                                                                                                                                  Length 715;
                                                                                                                                                                                                                                                                                                                65.3%; Score 2345.5; DB 4; Length 64.6%; Pred. No. 2.2e-154; ive 77; Mismatches 120; Indels
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                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 64.6
Matches 471; Conservative
                                                                                                                                                                                                                                                 the invention
                                                                                                                                                                                                                                                                                 Sequence 715 AA;
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71 QOYNPOGGYQOYNPQGGYQQQPNPQGGRGNYKNFNYNNN---LQGYQAGF-----QPQSQ 122 123 G------MSLNDFQKQQKQAA----PKPKKTLKL-VSSSGIKLANATKKVGTKPAES 168 DQQQETGSGQMSLEDYQKQQKESLNKLNTKPKKVLKLNLNSSTVKAPIVTKKKEEEPVNQ 211 QOEQOFGOYGOOONYNO-GGYNNYNNR----GGYSNNRGGYNNSNRGGYSNYN---SYN 108 TNSN-ÓGGYSNÝN-----NYVANNSÝNNNNNNNNNNÝNQGYNNYNSÓPÓGÓ DKKEEEKSAE---TKEPTKEPTKVEE-----Matches 433; 11 169 26 152 Query Match Local g g 셤 ઠે à ò ઠે 645 705 406 434 466 494 674 TINKEERINGKTIEVGKAYFETDKRRYTILDAPGHKMYVSEMIGGASQADVGILVISARKG SGKWKDLGTIVEGKIESGHVKKGTNLIMMPNKTPIEVLTIFNETEQECDTAFSGEQVRLK TNKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKG EYETGFERGGOTREHALLAKTOGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAI EYETGFEKGGQTREHALLAKTQGVNKI I VVVNKMDDSTVGWSKERYQECTTKLGAFLKGI GYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMNHVDRHINAPFMLPI **AAKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAMCGEQVKLR** IKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHI VKLLHKLEKGTNRKSKKPPAFAKKGMKVIAVLETEAPVCVETYQDYPQLGRFTLRDQGTT IAIGKIVKI 683 706 IAIGKITKL 714 347 407 467 495 586 646 375 615 675 435

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The specification describes chimeric polypeptides which comprise at least one SCHAG (self-coalesces into higher-order aggregates) amino acid sequence fused in frame with a polypeptide of interest (which is other than a marker protein, a glutathione-S-transferase or a staphylococcal nuclear protein). The specification also describes chimeric polypeptides that comprises an amyloidogenic domain that causes aggregation into miltiple reactivities, e.g. derivatised with ensymes, or specific binding partners, and useful e.g. for performing multi-step chemical reactions. They can be used create an inducible, or stable phenotypic alteration in a cell, e.g. for gene therapy, protein production, imparting disease resistance to plants, altering plant pigmentation and for diagnosis and treatment of prion diseases. The present sequence is used in the course
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding chimeric proteins with self-assembly properties, useful e.g. for diagnosis and treatment of prion diseases, also related aggregates, fibrils and polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQ
                                                                                                                                   SCHAG; self-coalesce; higher-order aggregate; amyloidogenic domain; aggregation; fibril; phenotypic alteration; gene therapy; disease resistance; plant pigmentation; prion disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Scheibel
                                                                                                                                                                                                                                                                                                                                                                                                                            Sondheimer N,
                                                                                                      Amino acid sequence of a Pichia pinus protein.
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AAB30819 standard; protein; 741
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                                                                                                                                                                                                             Pichia pinus.
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ESKTEEPAKEEIKNQEPAEAENKVEEESKVEAPTAAKPVSESEPPAST-PKTEAKASKEV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; card tolerance; nest tolerance; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                            FETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTREHALL
                                                    PKVEDLKI SESTHNTNNANVTSADALI KEQEEEVDDEVVNDMFGGKDHVSLI FMGHVDAG
                                                                                                                                                      KSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIEVGKAY
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HINKLE G J.
SLATER S C.
CHEN X.
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant comprising the transformed plant with the newing an improved property comprises transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant properties, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of photopyntessis or pass or pest phosphorus use and/or uptake, by modification of photopyntessis or property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
provide
   New recombinant DNA construct comprising a promoter positioned to provi for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                           Claim 1; SEQ ID NO 22730; 122pp; English
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57; Length 690; Indels 46.7%; Score 1679.5; DB 8; llarity 51.4%; Pred. No. 4.5e-108; Conservative 109; Mismatches 148; 3 Best Local Similarity Matches 332; Conserv Query Match

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Sequence 690 AA;

15;

Gaps

220 VGTKPAESDKKEEEKSAETKEPTKPETKVEEPVKKEEKPVQTEEKTEEKSELPKVEDLKI 191 원 a Š

LYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIEVGKAYFETEKRRY 340 231 281 g ò 8

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SESTHINTINNAINTSADALIKEQEEEVDDEVVNDMFGGKDHVSLIFMGHVDAGKSTMGGNL

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459 TILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNK 400 SLLDAPGHKGYVINMINGASQADIGVLVISARRGEFEAGFERGGQTREHAVLARTQGINH 406 MVVVVNKMDDPTVNWSKERYDQCVSNVSNPLRAI-GYNIKTDVVFMPVSGYSGANLKDHV 341 347 요 à

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 RGNYKNFNYNNNLOGYOA-----GFOPOSOGMSLNDFOKOOKOAAPKFKKTLKLVS 148
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          TKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKPPAFAKKG
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48.1%; Pred. No. 1.5e-106;
tive 97; Mismatches 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590 ELKSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKPPAFAKKGMKVIAVLETE 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection; cancer; contamination; biofilm; antibody; immune response.
RIIEKYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIEVGKAYFETEKRRYTILDAPGHK
                                                                                                                                                                                   368 TYVPSMISGAAQADVALLVISARKGEFETGFEREGQTREHAMLIKNNGINKLIVVVNKMD
                                                                                                                                                                                                                                                                                                                                                                 488 PSLLEHLDNMEIMDRNINAPFMLPISEKYNELGTWVMGKIESGHVKKGDTLLMMPNKHTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIKEQEEBVDDEVVNDMFGG-----KDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDK
                                                                                                                                                                                                                                                  MYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVVVVNKMD
                                                                                                                                                                                                                                                                                                                                         DPTVNWSKERYDQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTG
                                                                                                                                                                                                                                                                                                                                                                                                                                470 PTLLEYLDTMNHVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHIKKGOSTLLMPNKTAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fumigatus essential gene protein #708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650 APVCVETYQDYPQLGRFTLRDQGTTIAIGKIVKIAE 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|:| ::|| |||||||||:| |:||||: |:|
APICIERFEDYKMLGRFTLRDEGKTVAIGKVTKLIE 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eroshkin AM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ26050 standard; protein; 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zamudio
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27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-02990P.
09-UUL-2001; 2001US-031899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-2002; 2002WO-US013142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus fumigatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-093124/08.
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539 KKNATCIMMPNRTKVEIAALYGETEDEIATATCGDQVRMRLRGVEEEDLLPGFVLCSPKR 598

the invention relates to more purities. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. Eumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object (by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. funigatus. The polymorlectides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic comparing with DNA potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for isolate correlative receptors or ligands invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention 71 QQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAGFQPQSQGMSL--- 126 102 NQY---GGYNOHQ-----QQQYT---------QQQXT-129 130 PSAPAQPAQTAPKPASTASAAPVLSIGGASSSSAAPKTKVLSIGTPSPA-----S 179 180 NTPSGTTTPGDTMGSAAADAAAKVTASKAIEKTEKKAAASGKSSPTPTASGRSSPGRSSP 239 226 NTNNANVT -- SADALIKEQEEEVDDEVVNDMFG-GKDHVSLIFMGHVDAGKSTMGGNLLY 282 283 LTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIEVGKAYFETE---- 336 ÓTYÓQYG-GGYPQYG--QYGGYPAYDQQQGFGQY----GAYAQQPGGYNQI----YN 101 127 NDFQKQQKQAAPKPKKT-----LKLVSSSGIKLANATK--KVGT-KPAESDKKEEEKSA 177 QNYQQYSQNGNQQQGNNRXQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQ 70 invention relates to novel purified or isolated nucleic acids of 95; 6; Length 716; ETKEPTKEPTKVEEPVKKEEKPVQTEEKTEEKSELPKVEDLKIS----186; Indels 43.3%; Score 1557.5; DB (46.6%; Pred. No. 1.4e-99; iive 99; Mismatches 186. Disclosure; Page; 175pp; English Best Local Similarity 46.6 Matches 332, Conservative Sequence 716 AA; 1 178 Query Match 55

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--KRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTREHALLAK 394

TOGVNKMVVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGAN 454

KKGQSTLLMPNKTAVB1QN1YNBTENBVDMAMCGEQVKLR1KGVEEED1SPGFVLJSPKN

LKDHVDPKECPWYTGPTLLEYLDTMNHVDRHINAPFMLPIAAKWKDLGTIVEGKIESGHI 514

455

515

therapeutic use, as markers for host tissues in which the pathogenic corganisms invade or reside, for comparing with the DNA sequence of A. Cramignisms invade or reside, for comparing with the DNA sequence of A. Cramignisms to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify sequences of other related or distant pathogenic organisms to identify optential or hologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to 575 PIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKPPA 634 New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer. essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response. The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polymucleotides are useful for expressing recombinant protein for characterisation, ecreening or Lemieux SM; 683 FAKKGMKVIA----VLETEAPVCVETYQDYPQLGRFTLRDQGTTIAIGKIVKI Hu W, Aspergillus fumigatus essential gene protein #108. Eroshkin AM, Tishkoff D, Zamudio C, Disclosure, Page, 175pp; English. ABJ25450 standard; protein; 712 27-APR-2001; 2001US-0287066P. 05-JUN-2001; 2001US-029589P. 09-JUL-2001; 2001US-0303899P. 31-AUG-2001; 2001US-0316382P. 23-APR-2002; 2002WO-US013142. 23-APR-2001; 2001US-0285697P. (first entry) (ELIT-) ELITRA PHARM INC Fungicide; cytostatic; cancer; contamination; Aspergillus fumigatus WPI; 2003-093124/08. WO200286090-A2. 16-APR-2003 31-OCT-2002 599 635 ABJ25450; 629 Jiang B, 셤 g 8 8

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New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.

, Sato H, Ishii S; i K, Irie R, Tamechika Masuho Y;

Otsuki T, Wakamatsu A, Hio Y, Otsuka K, Nagai Otsuka M, Nagahari K, N

f, Sugiyama T, of, Isono Y, F

Isogai T, Yamamoto

Seki N,

WPI; 2003-723558/69. N-PSDB; ADM02046.

(REAS-) RES ASSOC BIOTECHNOLOGY

22-MAR-2002; 2002JP-00137785. 12-APR-2002; 2002EP-00008400

EP1347046-A1 24-SEP-2003

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                                                                                                                                       QTYQQYG-GGYPQYG-QYGGYPAYDQQQGFGQY----GAYAQQPGGYNQI----YN
                                                                                                                                                                QQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAGFQPQSQGMSL----
                                                                                                                                                                                       ------OPPROAAPVATOA
                                                                                                                                                                                                              NDFQKQQKQAAPKPKKT-----LKLVSSSGIKLANATK--KVGT-KPAESDKKEEEKSA
                                                                                                                                                                                                                                  PSAPAQPAQTAPKPASTASAAPVLSIGGASSSSAAPKTKVLSIGTPSPA-----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKPPA
                                                                                             Gaps
isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential of Aspergillus fumigatus of the invention
                                                                                            95;
                                                                                                                                                                                                                                                            ETKEPTKEPTKVEEPVKKEEKPVQTEEKTEEKSELPKVEDLKIS-----
                                                                      Length
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                                                                                            183;
                                                                     42.3%; Score 1519.5; DB 46.3%; Pred. No. 6.3e-97; ive 98; Mismatches 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein of the invention SEQ ID NO:3174
                                                                                                                                                                                       NQY---GGYNQHQ-----QQQYT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDTNKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISAR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321
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                                                                                                                                                                                                                                                                                                      The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention May have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotide ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAPPPP-----AGGAANNHGAGSGAGGRAAPVESSQEEQSLCEGSNSAVSMELSEPIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKEQEEEVDDEVVNDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 NGETEMSPEESWEHKEEISEAEP---GGGSLGDGRPPEESAHEMMEEEEEIPKPKSVVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMNHVDRHINAPFML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRIKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1364.5; DB 7; Length
Pred. No. 3.3e-86;
; Mismatches 169; Indels.
                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 3174; 305pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96;
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49.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel polynuclectide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 KVEEP-VKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKEQEEEV
 AVLVISARKGEFETGFEKGGQTREHAMLAKTAGVKHLIVLINKMDDPTVNWSNERYEECK
                                           485 HINAPFMLPIAAKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDM
                                                                                                                                                                                      VHTAIEEVHIVKLIHKLEKGTNRKSKKPPAFAKKGMKVIAVLETEAPVCVETYQDYPQLG
                                                                                                                                   545 AMCGEQVKLRIKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFSCVMH
                            425 SNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMNHVDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.7%; Score 1354.5; DB 8; Length 499; larity 52.5%; Pred. No. 1.2e-85; Conservative 89; Mismatches 139; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; psoriasis; diagnosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; SEQ ID NO 187; 3069pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Antipsoriatic protein sequence #93
                                                                                                                                                                                                                                                                   494
                                                                                                                                                                                                                                                                                                                                     standard; protein; 499
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RFTLRDEGKTIAIGKVLKL
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Best Local Similarity
Matches 262; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a method of diagnosing breast cancer in subject comprising contacting biological sample from subject with at least two different breast cancer-associated polypeptides (I) encoded by nucleic acid molecules (II) comprising sequence chosen from 42 fully defined sequences as given in specification, determining specific binding between (I) and agents in sample, where presence of the binding is diagnostic for breast cancer. The method is useful for diagnosing breast cancer in a subject. The sample is blood, lymph node fluid or breast discharge fluid. This is the amino acid sequence of a breast cancer antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 KVEEP-VKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKEQEEEV 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing breast cancer in subject by obtaining biological sample from subject, contacting sample with breast cancer-associated polypeptides, determining specific binding between polypeptides and agents in sample.
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                                                                                                                                                                                                                                            cancer; breast cancer diagnosis; breast cancer antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Chen
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52.5%; Pred. No. 1.2e-85;
ive 89; Mismatches 139; Indels
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                                                                                                                                                                                                                  Human breast cancer antigen seg id 46.
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                                                                                                                                   ADC35080 standard; protein; 499
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nes 262; Conservative
                                                                   KTIAIGKVLKL 629
                                         TTIAIGKIVKI 683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO polynucleotides and polypeptides, useful in useful in diagnosing treating an immune related disease, e.g. systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune response stimulation; antiallergic; antianaemic; antiarthritic; antiasthmatic; antidiabetic; antinflammatory; antipsoriatic; antithyroid; CNS; dermatological; gastrointestinal;
                                                                                                                                                                                                                                                                                                              AVLVISARKGEFETGFEKGGQTREHAMLAKTAGVKHLIVLINKMDDPTVNWSNERYEECK
                                                                                                                                                                                                EKIVPFLKKVGFNPKKDIHFMPCSGLTGANLKEOSD--FCPWYIGLPFIPYLDNLPNFNR
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                                                   DDEVVNDMFGG--KDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGR
                                                                                   QGWYLSWVMDTNKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGGASQADV
                                                                                                                                                                                                                                                                           GVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERYDQCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHTAIEEVHIVKLLHKLEKGTNRKSKKPPAFAKKGMKVIAVLETEAPVCVETYQDYPQLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP54304 standard; protein; 499
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Wood WI, Wu TD;
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N-PSDB; ADP54303.
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The present invention describes an isolated PRO nucleic acid (1). Also described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the circle of method polypeptide; (5) a chimeric molecule comprising the composition of matter comprising a polypeptide of (4); an agonist or antagonist of the polypeptide or an antibody that binds to the composition of matter comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a comprising an enthod of treating the polypeptide; (11) a method of disease or an inflammatory immune response in a mammal; (12) a method of identifying a compound that inhibits or containers the activity of or expression of a gene encoding a PRO polypeptide; and (13) a method of stimulating the immune response in a mammal. The containment of antialleragic, antialmanenic, antialtratic, antiallamment; response in emphrorropic, neuroprotective, osteopathic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid (1) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing an immune response: represent sequence represents a human contain inflamment of the present sequence represents a human contains.
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 arthritis, diabetes mellitus or asthma and
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52.5%; Pred. No. 1.2e-85;
tive 89; Mismatches 139
                                                       English
                                                     Claim 1; SEQ ID NO 280; 3009pp;
 rheumatoid
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stimulating an
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idiopathic inflammatory myopathy, Siggren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune haemolytic anaemia, autoimmune thrombocytopania, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangtis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, cosinophilic pneumonia, idiopathic plumonary fibrosis, hypersensitivity pneumonia, idiopathic plumonary fibrosis, hypersensitivity pneumonia, idiopathic plumonary fibrosis, hypersensitivity pneumonia, idiopathic sequence represents a PRO protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antiinflammatory, ammunouppressive, osteopathic, autidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatocropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                                                                                      PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
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  494
                                                                                                      ADP24765 standard; protein; 499
                                                                                                                                                                                                                              polypeptide SEQ ID NO:1943
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RFTLRDEGKTIAIGKVLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2002; 2002US-0423394P
                                                                                                                                                                                       (first entry)
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Wood WI;

37.7%; Score 1354.5; DB 8; Length 499;

Query Match

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                                                 425 SNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMNHVDR
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                                                                                                                                                                                                                                                           485 HINAPFMLPIAAKWKDLGTIVEGKIESGHIKKGOSTLLMPNKTAVEIQNIYNETENEVDM
                                KVEEP-VKKEEKPVOTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKEQEEEV
                                                                             247 DDEVVNDMFGG--KDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGR
                                                                                          S9 KPKSVVAPPGAPKKEHVNVVFIGHVDAGKSTIGGQIMYLTGMVDKRTLEKYERAKEKNR
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            Gaps
            9;
            Indels
; Pred. No. 1.2e-85; 89; Mismatches 139;
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 Best Local Similarity
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search; using sw model

Run on:

July 1, 2005, 18:06:15; Search time 40.0283 Seconds (without alignments) 1646.548 Million cell updates/sec

US-09-591-632-2 3594 1 MSDSNQGNNQQNYQQXSQNG......FTLRDQGTTIAIGKIVKIAE 685

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		or 2	ran	omnipotent nonsens	omnipotent nonsens	SUP35 protein - Af	suppressor 2 prote	D.	hypothetical prote		ă	-	translation elonga		translation elonga	translation elonga		_	translation elonga	translation elonga		_				translation elonga	$\overline{}$	Φ	translation elonga
	ID	K	\$12921	T51896	T41442	T51948	S58444	S06941	T03717	T23102	T03718	T43011	A49171	S54734	S11665	A54760	S35894	A35154	806300	S35772	JC5117	843507	S43861	A25938	T41617	835986	T38230	H90162	N	T42089
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	Length	685	741	729	662	662	614	499	515	573	409	280	435	441	456	449	458	458	458	460	449	435	460	458	460	457	460	435	459	460
<b>l</b> P (	Query	100.0	9.09	47.8	47.0	46.6	38.3	37.7	35.7	33.8	32.3	26.3	23.9	23.6			23.5	23.1	23.1	23.1	23.1	23.0	23.0	٠	ď	ö	22.9	22.8	22.8	22.8
	Score	3594	2177	1719	1689	1675	1375	1354.5	1283.5	1213.5	1160.5	946.5	859.5	847	844	836.5	833	831	829	829	828.5	826	825.5	N	N	•	2	821	2	819
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		translation elonga	protein T6D22.2 [i	probable translati	translation elonga	translation elonga	translation elonga								
T43267	JC4214	T47258	T44963	T43704	S16308	859595	T43894	S08534	S10507	S06724	F86214	C72570	EFBY1A	A60491	EFHUI
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460	460	460	444	461	446	459	460	449	448	449	196	437	458	462	462
22.7	22.7	22.6	22.6	22.5	22.4	22.3	22.3	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2
817	814.5	813.5	812	808.5	806.5	802	800	799.5	798.5	798.5	798.5	798	797.5	797	796.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

	RESULT 1
	suppressor 2 protein - yeast (Saccharomyces cerevisiae) N'Alternate names: G1-to-S transition protein; protein YD9395.05; protein YDR172w
	C;Species: Saccinatomyces Cerevisiae C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004 C;Accession: S00733; JT0323; \$49768; S00488; A26742; S00533; S05723 D:Wilcon D G . Cilbartean M D
	J. Mol. 199, 555-573, 1988 A; Title: SUF12 suppressor protein of yeast. A fusion protein related to the EF-1 family
	A;Kereferiore number: SU0/33; MU1D:881/2503; FM1D:328080/ A;Accession: S00733 A;Molecule type: DNA
	A, Residues: 1-685 sWil. A. A. A. A. A. A. A. A. C. A. A. C. J. FID: 94582 R; Kushnirov, V.V.; Ter-Avanesyan, M.D.; Telckov, M.V.; Surguchov, A.P.; Smirnov, V.N.; I
	Gene 66, 45-54, 1988 A;Title: Nucleotide sequence of the SUP2(SUP35) gene of Saccharomyces cerevisiae. A:Reference number: JT0323: MIID:88329727: PMID:3047009
••	A; Molecule type: DNA
	A;kesidues: 1-685 <kus> A;Cross-references: EMBL:M21129; NID:g172789; PIDN:AAA35133.1; PID:g172791</kus>
	R;Murphy, L.; Harris, D.E. submitted to the RMBL Data Library. November 1994
	A; Reference number: S49764
	A; Molecule type:
	AjkeBidues: 1-655 <muk> AjCross-references: EMBL:246727; NID:g1289283; PIDN:CAA86677.1; PID:g1289287; GSPDB:GN00 D.Wilmicht V. Chimatho H. Vilmicht A</muk>
	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
	A;Title: A yeast gene required for the G1-to-S transition encodes a protein containing a A;Reference number: S00488; WUID:88296422; PMID:2841115
	A;Accession: S00488 A;Molecule type: DNA
	A;Residues: 1-52,'C',54-685 <kik> A:Cross-references: GB:Y00829; EMBL:Y00859; NID:q3711; PIDN:CAA68760.1; PID:q3712</kik>
	C; Genetics:
	A,Cross-references: SGD:S0002579; MIPS:YDR172w
	A;Map position: 4R C:Sherfamily: suppressor 2 protein: translation elopostion factor Thi homology
	C; Keywords: duplication; GTP binding; nucleotide binding; P-loop; phosphoprotein; tandem
	F;1-12/John 10-residue repeats
	F;124-253/Domain: charged <dom2> F;159-222/Region: glutamic acid/lysine-rich</dom2>
	F;254-685/Domain: C < DOM4>
	F;261-409/Domain: translation elongation ractor in nomology <pre>F;267-274/Region: nucleotide-binding motif A (P-loop)</pre>
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C; Keywords: GTP binding;
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Suppressor 2 protein - yeast (Pichia pinus)

Nylternate names: SUP2 protein

C; Species: Pichia pinus

C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C; Date: 18-2921

R; Mushnirov, V.V.; Ter-Avanesyan, M.D.; Didichenko, S.A.; Smirnov, V.N.; Chernoff, Y.O.; Veast 6. 461-472, 1990

N; Machinitov, V.V.; Ter-Avanesyan, M.D.; Didichenko, S.A.; Smirnov, V.N.; Chernoff, Y.O.; Veast 6. 461-472, 1990

A; Accession: S12921

A; Accession: S12921

A; Molecule type: DNA

A; Residues: 1-741 «KUS>

A; Accession: S12921

A; Molecule type: DNA

A; Residues: 1-741 «KUS>

A; Coserice: C; Conecice: NIPROT: P23637; EMBL: X56910; NID: G3235; PIDN: CAA40231.1; PID: G3236

C; Genetics: A; Gene
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                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                           420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVDRHINAPFWLPIAAKWKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETEN 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                       SQCMSLNDFQKQQKQAAPKPKKTLKLVSSSGIKLANATKKVGTKPAESDKKEEEKSAETK 180
                                                                                                                                                                                                                                                                                                                          EPTKEPTKVEEPVKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIK 240
                                                                                                                                                                                                                                                                                                                                                                                                 EQEEEVDDEVVNDMFGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYERAK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAGROGWYLSWVMDTNKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGGAS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVVVNNKMDDPTVNWSKERY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMN 480
                                                                                                                                                                                                                   QOYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAGFQPQ 120
                                                                                                                                                                                                                                                    SQGMSLNDFQKQQKQAAPKPKKTLKLVSSSGIKLANATKKVGTKPAESDKKBEEKSAETK 180
                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVDMAMCGEQVKLRIKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFS
                                                                                                                                            MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGY
                                                                                                           1 MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGY
                                                                        Gaps
                                                                        ö
                                     Length 685;
                                                                      Indels
                                   100.0%; Score 3594; DB 1; 100.0%; Pred. No. 1.1e-178;
                                                                      0; Mismatches
   (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        685
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   GTP
                                   Query Match
Best Local Similarity
Matches 685; Conserv
     site:
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 F;273/Binding
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RESULT 3

Trobable translation release factor erf3 [imported] - Neurospora crassa

N.Alternate names: protein B23111.80

C;Species: Neurospora crassa
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000

C;Accession: T51896

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitteed to the Protein Sequence Database, August 2000

A;Reference number: Z25858
A;Accession: T51896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQQQETGSGQMSLEDYQXQQKESLNKLNTKPKKVLKLNLNSSTVKAPIVTKKKEEEPVNQ 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABAAAALKKEVSQAKKESINVTNADALVKEQEEQIDASIVNDMFGGKDHMSIIFMGHVDAG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSTWGGNILYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIEVGKAY 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   632
                                                                                                                                                                                                                                                                                                                                                                   QQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNYNNN---LQGYQAGF-----QPQSQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- PVKKEEKPVQTEEKTEEKS--EL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKTOGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSG 452
                                                                                                                                                                                                                                                                                                              QOBQOFGOYGQQQQNYNQ-GGYNNYNNR----GGYSNNRGGYNNSNRGGYSNYN---SYN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-----MSLNDFQKQQKQAA----PKPKKTLKL-VSSSGIKLANATKKVGTKPAES 168
                                                                                                                                                                                                                                                                                                                                                                                                                       TNSN-QGGYSNYN------NYASYNNNNYNNNYNNYNQGYNNYNSQPQGQ 151
                                                                                                                                                                                                                                                                70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       573 KNPIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGOTREHALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANLKDHVDPKECPWYTGPTLLEYLDTWNHVDRHINAPFMLPIAAKMKDLGTIVEGKIESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIKKGOSTLLMPNKTAVBIQNIYNETENEVDMAMCGEQVKLRIKGVEBEDISPGFVLTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 PKVEDLKISESTHNTNNANVTSADALIKEQEEEVDDEVVNDMFGGKDHVSLIFMGHVDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAFAKKGMKVIAVLETEAPVCVETYQDYPQLGRFTLRDQGTTIAIGKIVKI 683
                                                                                                                                                                                                           64;
nucleotide binding; P-loop; phosphoprotein ation elongation factor Tu homology <ETU>
                                                                                                                                                       Length 741;
                                                                                                                                                                                                           Indels
                                                                                                                                                    Query Match 60.6%; Score 2177; DB 2;
Best Local Similarity 60.9%; Pred. No. 2.6e-105;
Matches 433; Conservative 87; Mismatches 127;
                      F;319-467/Domain: translation elongation factor Tu ho F;325-332/Region: nucleotide-binding motif A (P-loop) F;464-467/Region: GTP-binding MSCD motif F;331/Binding site: GTP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 DKKEEEKSAE---TKEPTKVEE-----
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us-09-591-632-2.rpr

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A; Molecule type: DNA
A; Readdues: 1-662 <SES.
A; Cross-references: UNIPROT:074718; EMBL:AL032824; PIDN:CAA21821.1; GSPDB:GN00068; SPDB:
A; Experimental source: strain 972h-; cosmid c584
C; Genetics:
A; Gene: SPDB:SPC584.04
A; Map position: 3
A; Introns: 44/1
C; Superfamily: suppressor 2 protein; translation elongation factor Tu homology
F; 239-387/Domain: translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                             122 QGMSLN-----DFQKQQKQAAPKPK----KTLKL------VSSSGIKLAN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                 157 ATKKVGTKPAESDKKEEEKSAETKEPTKEPTKVEEPVKKEEKPVQTEEKTEEKSELPKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTKPAA--PAAQSKTETPAPKVTSESTKKETAAPPP---QETP--TKSADAELAKTPSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SNOPNNGEQDEQLAKQTSKLSMSAKAPTFTPKAAPFIPS------FQRPGFVPV
                                                                                                                                                                                                                                                                                                                                                  64 NPDAGYQQQYNPQGG--YQQYNPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAGFQPQS
                                                                                                                                                                                                                                                                                                                                                                                51 N-----NIAGGYPYAQYTGQG------ONSNSPHPTKSYQQYYQ-KP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLKISESTHNTNNANVTSADALIKEQEEEVDDEVVNDMFGGKDHVSLIFMGHVDAGKSTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIEVGKAYFETE
                                                                                                                                                                                                                                                                                    4 SNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQY
                                                                                                                                                                                                                     47.0%; Score 1689; DB 2; Length 6 48.2%; Pred. No. 4.1e-80; Ative 121; Mismatches 169; Indels
                 A;Accession: T41442
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                       Conservative 121;
   A; Reference number: Z21993
                                                                                                                                                                                                                                       al Similarity
342; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217
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Matches 34
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Omnipotent nonsense suppressor, ef1 alpha factor-like gtp-bindingprotein - fission yeast C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Accession: T41442
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
                                                                                                                                                                                                                                                                                  62 YÓQÓYYGGAQÓGYGGGYPQYGQQGYGQYNNQ--QÓÓGYGAVYGQÓGYNQGYGQQQQQQ 119
                                                                                                                                                                                                                                                                                                                                                120 QQYGGYQQNQGYQQRQQQNRDAPKPAPQIVKRPEQPAAQAQPKADAPKTAAAPVKVLSVG 179
                                                                                                                                                                                                                                                                                                                                                                             ----KLVSSSGIKLANATKKV---GTKPAESDKKEEEKSAETKEPTKEPTKVEEPVKKE 196
                                                                                                                                                                                                                                                                                                                                                                                                GGKDHVSLIFMGHVDAGKSTMGCNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GKEHMNIIFIGHVDAGKSTLGGAILYVTGMVDQRTLDKYKREAKDMGRETWYLSWALDL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKEERNDGKTIEVGKAYFETEKRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YETGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMNHVDRHINAPFMLPIA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :|:|||:|||||:|||||:||||:||| | SYXRDMGTMIEGKIEAGVEVEVGEGVELLEL 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALLHKLQKGTNRKSKLPPSHAKKGDSIIARLEVTGGAGSVCVERFEDYPQMGRFTLRDQG 712
                                                                                                                                                                                                                                                                                                                 GGRGNY-KNFNYNNNLQGYQAGFQPQSQGMSLND---FQKQQKQAAPK----PKKTL--- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAMCGEQVKLRI 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHIV 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLIHKLEKGTNRKSKKPPAFAKKGMKVIAVLET---EAPVCVETYQDYPQLGRFTLRDQG 672
                                                                                               homology
                                                                                                                                                                                          .---- 37
                                                                                                                                                                                                                       61
                                                                                                                                                                                                                       GNVÓNNWEBAADODERLARÓTOQOMNINAGTFR-PGAAAFTPGAPSFTPGQFAAPGFTPQ
                                                                                                                                                                                                                                                     -QAQPAGGYYQNY-QGYSGYQQGGYQQYNPDAGYQQQYNPQGGYQQYNPQGGYQQYNPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                            EKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKE-QEEEVDDEVVNDMF
                                                                                                                                                           Gaps
                                                                                               뎚
                                                                                                                                                           64;
                                                                                               factor
                                                                                                                          DB 2; Length 729;
 Cross-references: EMBL:AL391572; GSPDB:GN00116; NCSP:B23111.80
Experimental source: BAC clone B23111; strain OR74A
                                                                                                                       47.8%; Score 1719; DB 2; Length 7
49.9%; Pred. No. 1.3e-81;
live 98; Mismatches 204; Indels
                                                                                            protein; translation elongation
                                                                                                                                                                                        GNNQQNYQ-----QYSQNGNQQQGNNRYQGYQAYNA---
                                                                                                                                                        365; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTIAIGKIVKI 683
                                                                            Introns: 111/1; 711/3; Superfamily: suppressor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTIAIGKITKL
A; Cross-references: EMBL
A; Experimental source: B
C; Genetics:
A; Gene: NCSP: B23111.80
A; Map position: 6
A; Introns: 111/1; 711/3
C; Superfamily: suppresso
                                                                                                                                         Similarity
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336

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78;

Length 662;

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pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  omnipotent nonsense suppressor SUP35/eRF-3 - fission yeast (Schizosaccharomyces C; Species: Schizosaccharomyces pombe
C; Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C; Accession: T51948
                                                   396
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KDHVDPKECPWYTGPTLLEYLDTWNHVDRHINAPFMLPIAAKWKDLGTIVEGKIESGHIK
                                                   337 KRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQ
                                                                                                                          GVNKMVVVNKMDDPTVNMSKERYDQCVSNVSNFLRAI-GYNIKTDVVFMPVSGYSGANL
                                                                                                                                                                                                                                 KDRVDSSVCPWYQGPSLLEYLDSMTHLERKVNAPFIMPIASKYKDLGTILEGKIEAGSIK
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276

KRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQ 396

GGNILYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIEVGKAYFETE 336

277 206 337

149

VGTKPAESDKKEEEKSAETKEPTKEPTKVEEP-VKKEEKPVQTEEKTEEKSELPKVEDLK 219

99; Mismatches 148; 38.3%; Score 1375; DB 2; 50.5%; Pred. No. 6.5e-64;

Conservative

161 93 220

Similarity

ISESTHINTINNANVTSADALIKEQEEEVDDE---VVNDMFGGKDHVSLIFMGHVDAGKSTM

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Virtnessary of J. Frolova, L.; le Goff, X.; le Guellec, R.; Inge-Vechtomov, S.; Kisselev EMBO J. 14, 4065-4072, 1995
A.Tille: Termination of translation in eukaryotes is governed by two interacting polypept A; Reference number: S58444
A; Reference number: S58444
A; Reference number: S58444
A; Reference number: S58445
A; Reference number: S58445
A; Residues: Preliminary
A; Residues: 1-614 cZHO>
A; Cross-references: UNIPROT: 091855; EMBL: L37045; NID: 9976218; PIDN: AAC42228.1; PID: 997621
A; Cross-references: UNIPROT: 091855; EMBL: L37045; NID: 9976218; PIDN: AAC42228.1; PID: 997621
C; Superfamily: suppressor 2 protein; translation elongation factor Tu homology
C; Superfamily: suppressor 2 protein; translation elongation factor Tu homology
C; Superfamily: suppressor 2 protein; translation elongation factor Tu homology
C; Superfamily: suppressor 2 protein; translation elongation factor Tu homology
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C; Superfamily: suppressor 2 protein; translation factor Tu homology
C; Superfamily: suppressor 2 protein; translation factor Tu homology
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Best Local Simil
Matches 266; C
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R;Ito, K.; Ebihara, K.; Nakamura, Y.

RNA 4, 958-972, 1998

RNA 4, 958-972, 1998

RNA 4, 958-972, 1998

RNA 4, 958-972, 1998

RA; Title: The stretch of C-terminal acidic amino acids of translational release factor A; Reference number: 225883

A; Reference number: 225883

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Rocale type: DNA

A; Residues: 1-62 < ITO>

A; Residues: 1-62 < ITO>

A; Residues: 1-62 < ITO>

A; Cross references: UNIPROT: 074718; EMBL: D79214; PIDN: BAA33530.1

A; Resperimental source: strain J7333

C; Genetics:
A; Af, 1

C; Superfamily: suppressor 2 protein; translation elongation factor Tu homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 KRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQ 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 TIKPAA--PAAQSKIETPAPKVISESIKKETAAPPP---QETP--TKSADAELAKTPSAP 198
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46.6%; Score 1675; DB 2; Length 6
Best Local Similarity 47.9%; Pred. No. 2.1e-79;
Matches 340; Conservative 121; Mismatches 171; Indels
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                                                                                                                                                                                                                                                                                                                                 Nighternate names: GST1 protein homolog
Nighternate names: GST1 protein homolog
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S06941
R;Hoshino, S.I.; Miyazawa, H.; Enomoto, T.; Hanaoka, F.; Kikuchi, Y.; Kikuchi, A.; Ui,
EMBO J. 8, 3807-3814, 1989
A;Title: A human homologue of the yeast GST1 gene codes for a GTP-binding protein and A;Reference number: S06941; MUID:90059983; PMID:2511002
A;Accession: S06941
HSGRTFDAQIVIIEHKSIICPGYNAVLHIHTCIEEVEITALICMVDKKSGEKSKTRPRFV 562
                                                                                 suppressor 2 protein homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-499 <HOS>
                          503
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S58444
SUP35 protein - African clawed frog (fragment)
SUP35 proteis: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004

636

577 KSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKPPAFA

GOSTLIMPNKTAVEIQNIYNETENEVDMAMCGEQVKIRIKGVEEEDISPGFVLTSPKNPI 576 

DHVDPKECPWYTGPTLLEYLDTWNHVDRHINAPFMLPIAAKWKDLGTIVEGKIESGHIKK 516

GVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGANLK 456

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Query Match Best Local S

Matches

365

119

239 485

999

Match

Query

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A;Cross-references: UNIPROT:045622; EMBL:292835; PIDN:CAB07395.1; GSPDB:GN00023; CBSP:H1
A;Experimental source: clone H19N07
C;Genetics:
                              7.
                                                                                                                                                                                                                                                                                                  353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 NATKKVGTKPAESDKKEEEKSA-----ETKEPTKBPTKVEEPVKKEEKPVQTEEKTEEK 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apporbatical protein H19N07.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23102
R;Dobson, R.
submitted to the EMBL Data Library, March 1997
A;Accession: T23102
A;Accession: T23102
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                       235 ADALIKEQEBEVDDEV-VNDMFGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIE
                                                                                   EPTKVEEPVKKE----EKPVQTEEKTEEKSELPKVEDLKISESTH-----NTNNANVTS
                                                                                                                                                                                                                                                                                                  KYEREAKDAGROGWYLSWVMDTNKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVS
                                                                                                                                                                                                                                                                                                                                                                                                                                        178 NMISGRSQADIGLLVISARKGEFETGYERGGTREHVQLAKTLGVTKFLVVVNNOMDDPTV
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                              21;
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33.8%; Score 1213.5; DB 2; Length 573;
Best Local Similarity 39.6%; Pred. No. 1.4e-55;
Matches 252; Conservative 115; Mismatches 158; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP:H19N07.1
A; Map position: 5
A; Map position: 5
C; Superfamily: suppressor 2 protein; translation elongation factor F;110-258/Domain: translation elongation factor
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                              Indels
  2.8e-59;
ches 148;
  Pred. No. 2.8e-
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89;
     ilarity 49.6%;
Conservative 6
     Local Similarity
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T03117
GTP-binding protein SUP1, EF-1-alpha-related - common tobacco
C; Species: Nicotiana tabacum (common tobacco)
C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C; Accession: T03117
R; Brander; K.A.; Owttrim, G.W.; Brunold, C.
Plant Physiol. 108, 1748, 1995
A; Title: Isolation of a cDNA (EMBL X85803) encoding a putative chloroplastic isoform of A; Receivence number: 215026
A; Accession: T03717
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T03717
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T03717
A; Status: preliminary; translated from GB/EMBL, DDBJ
A; Coss-references: UNIPROT: Q40581; EMBL: L38828; NID: 91009231; PIDN: AAA79032.1; PID: 9106
A; Experimental source: strain SR1
C; Genetics:
A; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 VAPGENLKIRLKGIEEEEILPGFILCDPNNLCHSGRTFDAQIVIIEHKSIICPGYNAVLH
                                                                                                                                                                                                                                                                                                  188 KVEEP-VKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKEQEEEV
                                                                                                                                                                                                                                                                                                                                                                                                         DDEVVNDMFGG--KDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGR
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                                                                                                                                                                                                                                               Gaps
C;Superfamily: suppressor 2 protein; translation elongation factor Tu C;Keywords: GTP binding; nucleotide binding; P-loop F;75-223/Domain: translation elongation factor Tu homology <ETU>F;81-88/Region: nucleotide-binding motif A (P-loop) F;220-223/Region: GTP-binding NKXD motif F;87/Binding site: GTP (Lys) #status predicted
                                                                                                                                                                                                                                             6
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                                                                                                                                                                                          Length
                                                                                                                                                                                        37.7%; Score 1354.5; DB 2; Length 52.5%; Pred. No. 5.7e-63; ive 89; Mismatches 139; Indels
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                                                                                                                                                                                                                                             262; Conservative
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C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolo C;Superfamily: translation elongation factor Tu homolo C;Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis f.21-21-60/Domain: translation elongation factor Tu homology <FTU>F;18-25/Region: nucleotide-binding motif A (P-loop)
F;187-160/Region: GTP-binding NKXD motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation elongation factor eEF-1 alpha chain - slime mold (Dictyostelium discoideum)
NyAlternate names: actin-binding protein ABP-50
Sipecies in Dictyostelium discoideum
C;Deces: Dictyostelium discoideum
C;Date: 12-Feb-1993 #sequence revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: S11665; S36934; S36935
Nature 347, 494-496, 1990
Nature 347, 494-496, 1990
A;Title: identification of an actin-binding protein from Dictyostelium as elongation fac A;Reference number: S11665; MUID:91015340; PMID:2215665
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A;Residues: 9-17;138-149;162-166;418-421 <YAF>
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolc C;Keywords: actin binding; blocked amino end; GTP binding; nucleotide binding; P-loop; p
F;11-159/Domain: translation elongation factor Tu homology <ETU>
F;11-24/Region: nucleotide-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGFERGGOTREHALLAKTOGVNKMVVVNKMDDPTVNWSKERYDOCVSNVSNFLRAIGYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496 AKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETEN-EVDMAMCGEQVKLR
                                                                                                                                                                                                                                                                                                                                                                                                                   258 KDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNK
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A;Experimental source: strain AX-3; clone 50-1.5
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6
                                                                                                                                                                                                                                                                           ; Score 847; DB 2; Length 44; Pred. No. 8.9e-37; 99; Mismatches 154; Indels
                                                                                                                                                                                                                                                                           23.6%;
                                                                                                                                                                                                                                                                                                                                                 Matches 168; Conservative
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A; Residues: 1-453 < YAN>
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A; Residues: 7-456 < YAW>
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                                             codon: GTG
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A;Reference number: A49171; MUID:93049915; PMID:1385189
A;Accession: A49171
A;Molecule type: mRNA
A;Residues: 1.435 KUR>
A;Accession: E49171
A;Note: sequence extracted from NCB1 backbone (NCBIN:117509, NCBIP:117510)
A;Accession: B49171
A;Note: sequence extracted from NCB1 backbone (NCBIN:117509, NCBIP:117510)
A;Accession: B49171
A;Molecule type: protein
A;Residues: 2-21 kMU2>
C;Genetics:
A;Genetics:
A;Genetics: A;Genetics:
C;Genetics: A;Genetics: A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 GGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 NKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YETGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | : |:||:|| |: | |: | XKPDT-IPFIPEPPKRPUDKPLRLFLQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 NIKGVSVKDIRRGNVASDAKNDPAKBATFYSQVIIMNHPGQIQAGYTPVLDCHTAHIAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTWNHVDRHINAPFMLPI- 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -AAKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAMCGEQVKL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -IEEVHIVKLLHKLEKGTNRKSKKPPAFAKKGMKVIAVLETEAPVCVETYQDYPQLGRFT 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
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A;Residues: 1-441 <CEC>
A;Cross_references: EMBL:X73582
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDKVHINLVVIGHVDSGKSTTTGHLIYKCGIDKRVIEKFEKESAEQGKGSFKYAMVLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKGVEEEDISPGFVLTSPKN-PIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.9%; Score 859.5; DB 2; 39.9%; Pred. No. 2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91; Mismatches 154;
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A,71161: Procein translation elongation factor-lalpha from Trypanosoma brucei binds calm A,Reference number: A54760; MUD:94364999; PMID:8083206

A,Recession: A54760

A,Recession: A54760

A,Residues: 1-239, 'TCT', 243-449 «KAU>
A,Robecule trype: MRNA

A;Residues: 1-239, 'TCT', 243-449 «KAU>
A;Robecule trype: MRNA

A;Residues: 1-239, 'TCT', 243-449 «KAU>
A;Robecule trype: As and fungi are each other's closest relatives: congruent evidence from m A;Reference number: A49394; MUD:94089672; PMID:826589

A;Title: Animals and fungi are each other's closest relatives: congruent evidence from m A;Reference number: A49394; MUD:94089672; PMID:826589

A;Statuus: preliminary; nucleic acid sequence not shown; translation not shown A;Nolecule trype: DNA

A;Residues: 18-418 «ABL.
A;Residues: 18-418
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                                                                                                                                                         258 KDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNK 317
                                                                                                                                                                                                                                                                                          68 AERERGITIDIALWKFETSKYYFTIIDAPGHRDFIKNMITGTSQADCAVLVIASPTGEFE 127
                                                                                                                                                                                                                                                                                                                                                                                              - PEKVAFVPISGWNGDNMLERSDKME--WYKGPTLLEALDAIVEPKRPHDKPLRIPLODV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAMCGEQVKLRI 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 YKIGGIGTVPVGKVETGIIKPGMVVTPAPAGLSTEVKSVEMHHE-QLPEARPGDNVGFNV 303
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                                                                                                                                                                                                                                                                                                                                                                   TGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGYN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMNHVDRHINAPFMLPI--A 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGVEEEDISPGFVLTSPKN-PIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHI 614
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                                                     Length 456;
                                                Similarity 41.0%; Pred. No. 1.38-36; Length 45 Similarity 41.0%; Pred. No. 1.38-36; Conservative 82; Mismatches 161; Indels
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F;156-159/Region: GTP-binding NKXD motif
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RQTVAVGVI 432
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                                                                           TGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGYN 437
                                                                                                                                                                                    IKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMNHVDRHINAPFMLPI--A 495
                                                                                                                                                                                                                                                                                                              KGVEEEDISPGFVLTSPKN-PIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHI 614
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                615 VKLLHKLEKGTNRKSKKPPAFAKKGMKVIAVLETEAPVCVETYQDYPQLGRFTLRDQGTT
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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GenCore version 5.1.6
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                                                                                                                                 July 1, 2005, 18:17:24; Search time
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US-09-949-016-7704

US-08-371-377-18

US-08-875-553D-24

US-08-371-377-17

US-08-371-377-17

US-08-371-377-19

US-08-875-553D-23

US-08-875-553D-25
                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
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Match
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473.5
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Maximum DB E
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No.
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ICE 19826, 4		57	ıce 3, Appli	70	ice 24554, A	ice 19849, A	ıce S, Appli		ice 15559, Ā	ıce 2, Appli	ice 4, Appli	79,	ice 76, Appl		ice 3, Appli		ice 3408, A
Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-248-796A-19826	US-09-489-039A-10194	US-09-328-352-5741	US-09-962-357-3	US-09-543-681A-7087	US-09-252-991A-24554	US-09-248-796A-19849	US-09-140-466-5	US-09-134-001C-5377	US-09-902-540-15559	US-09-218-197-2	US-09-140-466-4	US-09-598-401C-79	US-09-438-185A-76	US-09-198-452A-90	US-09-140-466-3	US-09-710-279-1312	US-09-583-110-3408
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177	478	538	433	496	652	176	409	414	396	394	408	136	398	394	409	310	398
12.7	11.9	11.7	10.8	10.8	10.8	10.3	6.6	9.6	7.6	9.7	9.5	9.4	9.3	9.3	9.5	9.5	9.1
455	427.5	419.5	389.5	389	387	369	357	351.5	349.5	348.5	340.5	337	335	332.5	331	330.5	328.5
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## ALIGNMENTS

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j Sequence 11158

j Sequence 11158

j Requence 11158

g GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-90-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 1158

LENGTH. 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 GGGSLGDGRPPEESAHBMMEEEEEIPKPKSVVAPPGAPKKEHVNVVFIGHVDAGKSTIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 GTKPAESDKKEEEKSAETKEPTKEPTKVEEP-VKKEEKPVQTEEKTEEKSELPKVEDLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 SESTHNTNNANVTSADALIKEQEEEVDDEVVNDMFGG--KDHVSLIFMGHVDAGKSTMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 NLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIEVGKAYFETEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKMVVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.0%; Score 1365.5; DB 4; Length 714; 50.9%; Pred. No. 4.4e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 4.4e-111; 94; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.99
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human
US-09-949-016-11158
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178 ETKEPTKEPTKVEEPVKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADA 237
                                                                   476 LDTMNHVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIY 535
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                                                                                                                                                                                                                                           416 SKERYDOCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEY 475
                                                                                                                                                                                                                                                                                                        596 AAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKPPAFAKKGMKVIAVLETEAPVCVE 655
170 IGGASQADLAVLVISARKGEFETGFEKGGQTREHAMFGKTAGVKHLIVLINKMDDPTVNW 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536 NETENEVDMAMCGEOVKLRIKGVEBEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.4%; Score 1307.5; DB 3; Length 499; 49.4%; Pred. No. 3.1e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Masaco, HORLE
APPLICANT: Toyomasa, KATAGIRI
TITLE OF INVENTION: HUMAN GENE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COMPRY: United States
CONTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/055,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.1e-106;
; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                      |::|:||:||:||:||
TFKDFPQMGRFTLRDEGKTIAIGKVLKL 494
                                                                                                                                                                                                                                                                                                                                                                                                  656 TYQDYPQLGRFTLRDQGTTIAIGKIVKI 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40, Application US/09055699; Patent No. 6005088; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFCATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/820,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94;
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tsutomu, FUJIWARA APPLICANT: Takeshi, WATANABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acid
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Matches 251; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 MMEEKEEIRKSKSVIVPSGAPKKEHVNVVFIGHVDAGKSTIGGQIMFLTGMADKRTLEKY 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | IGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVVVVKNKMDDPTVVW 415
519 STLLMPNKTAVEIQNIYNETENEVDMAMCGEQVKLRIKGVEEEDISPGFVLTSPKNPIKS 578
                                                                                            S46 QLVMMPNKHNVEVLGILSD-DVETDTVAPGENLKIRLKGIEEEEILPGFILCDPNNLCHS 604
                                                                                                                                                         579 VTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKPPAFAKK 638
                                                                                                                                                                                  605 GRIFDAQIVIIEHKSIICPGYNAVLHIHTCIEEVEITALICLVDKKSGEKSKTRPRFVKQ 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 ETKEPTKEPTKVEEPVKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADA 237
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                                                                                                                                                                                                                                                                   639 GMKVIAVLETEAPVCVETYQDYPQLGRFTLRDQGTTIAIGKIVKI 683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tsutcomu, FUJIWARA
APPLICANT: Takeshi, WATANABE
APPLICANT: Masato, HORIE
APPLICANT: Mosato, HORIE
APPLICANT: Toyomasa, KATAGIRI
TITLE OF INVENTION: HUMAN GENE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: United States
ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.4%; Score 1307.5; DB 2;
49.4%; Pred. No. 3.1e-106;
tive 94; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/820,170A
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40, Application US/08820170A
Patent No. 5831058
GENERAL INFORMATION:
APPLICANT: Talcomu, FUJIWARA
APPLICANT: Takeshi, WATANABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 499 amino acids
amino acid
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TELEX: 6491103
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERLETICS:
LENGTH: 499 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                           -08-820-170A-40
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Matches 25
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GENERALL INFORMATION:

GENERALL INFORMATION:

APPLICANT: HATANABE, TAKESHI

APPLICANT: HATANABE, TAKESHI

APPLICANT: HATANABE, TAKESHI

APPLICANT: HOUSE, MASATO

TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUWAN

TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME

TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME

TITLE OF INVENTION: 25.5359

CURRENT PAPLICATION NUMBER: 09/055,538

CURRENT FILING DATE: 1999-03-22

PRIOR APPLICATION NUMBER: 08/055,699

PRIOR FILING DATE: 1998-04-07

PRIOR FILING DATE: 1998-04-07

PRIOR PELING DATE: 1995-03-19

PRIOR FILING DATE: 1996-03-19

PRIOR FILING DATE: 1999-03-05

NUMBER OF SEQ ID NOS: 95

NUMBER OF SEQ ID NOS: 95
                                           IGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNW 415
                                                                                                                                                                                      475
                                                                                                                                                                                                            LDTMNHVDRHINAPFMLPIAAKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIONIY 535
                                                                                                                                                                                                                                                                                             SD-DTETDFVAPGENLKIRLKGIEEEEILPEFILCDPSNLCHSGRTFDVQIVIIEHKSII 406
                                                                                                                                                                                                                                                                                                                                                                                                                                           596 AAGFSCVMHVHTAIEEVHIVKLIHKLEKGTNRKSKKPPAFAKKGMKVIAVLETEAPVCVE 655
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                   EREAKDAGROGWYLSWVMDTNKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEM
                                                                                                                          NETENEVDMAMCGEQVKLRIKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSII
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36.4%; Score 1307.5; DB 3;
Best Local Similarity 49.4%; Pred. No. 3.1e-106;
Matches 251; Conservative 94; Mismatches 146;
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; Patent No. 6333404
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APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REPERBENCE: 0-5359
CURRENT APPLICATION NUMBER: US/09/273,565A
CURRENT FILING DATE: 1999-03-22
EARLIER APPLICATION NUMBER: 09/055,699
EARLIER APPLICATION NUMBER: 08/820,170
EARLIER APPLICATION NUMBER: 08/820,170
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
SEQ ID NO 40
SEQ ID NO 40
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LIKEQEE--EVDDEVVNDMFGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKY
                                                                              EREAKDAGRQGWYLSWVMDTNKEERNDGKTIEVGKAYPETEKRRYTILDAPGHKMYVSEM
                                                                                                                                                                  IGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVVVVVNKMDDPTVNW
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TPKDFPQMGRFTLRDEGKTIALGKVLKL 494
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: WATANABE, TAKESHI
APPLICANT: HORIE, MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REFERENCE: 0-5359
CURRENT APPLICATION NUMBER: US/09/976,165
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 09/65,538
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR APPLICATION NUMBER: 09/055,699
PRIOR PRILING DATE: 1997-03-19
PRIOR PELING DATE: 1997-03-19
PRIOR FILING DATE: 1997-03-19
PRIOR FILING DATE: 1997-03-19
PRIOR FILING DATE: 1997-03-19
SPRIOR FILING DATE: 1997-03-05
SOFTWARE: PACENTION NUMBER: JP 69163/1997
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PACENTIN VOY: 2.1
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                        GIERYEECKEKLVPFLKKVGFSPKKDIHFMPCSGLTGANIKEQSD--FCPWYTGLPFIPY
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                                                                                                                                                                                                                                                                                                             536 NETENEVDMAMCGEQVKLRIKGVEREDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSII
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Sequence 40, Application US/09976165
Patent No. 6562947
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: WATANABA, TSUTOMU
APPLICANT: WATANABA, TSUTOMU
APPLICANT: HOLECULE TAKESHI
APPLICANT: HOLECULE MAISOLATED
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING HUMAN
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REPREBENCE: 0-5359
CURRENT APPLICATION NUMBER: 09/055,699
FRIOR FILING DATE: 1998-04-07
FRIOR APPLICATION NUMBER: 09/055,699
FRIOR FILING DATE: 1997-03-19
FRIOR FILING DATE: 1996-03-19
FRIOR FILING DATE: 1996-03-19
FRIOR FILING DATE: 1996-03-19
FRIOR FILING DATE: 1997-03-05
FRIOR APPLICATION NUMBER: JP 69163/1997
FRIOR FILING DATE: 1997-03-05
                                                                                                       536 NETENEVDMAMCGEQVKLRIKGVEEBDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSII 595
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TFKDFPQMGRFTLRDEGKTIAIGKVLKL 494
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; Patent No. 6376189
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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Sequence 19819, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 PKT-VPFVPISGWNGDNM---IEPSTNCPWYKGWEKETKSGKVTGKTLLEAIDAIEPPTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543 DMAMCGEQVKLRIKGVEEEDISPGFVLTSPKN-PIKSVTKFVAQIAIVELKSIIAAGFSC
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                                                                                                                                                                                                                                                                                                                                                                                           Length 460;
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 1400 Mercantile Bank Tower, 1101 Walnut St.
CITY: Kanasa City
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                       23.1%; Score 831; DB 4; L
39.0%; Pred. No. 2.3e-64;
Live 87; Mismatches 160;
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                                                                                                                                                                                                                                                                                                                                   Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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US-09-248-796A-19819
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Best Local
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Matches
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Sequence No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR PLING DATE: 1999-02-13
PRIOR PLING DATE: 1998-02-13
PRIOR PLING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
     415
                                                                                           LDTWNHVDRHINAPFMLPIAAKWKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIY 535
                                                                                                                                                                    536 NETENEVDMAMCGEQVKLRIKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSII 595
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SD-DTETDFVAPGENLKIRLKGIEBEBILPBFILCDPSNLCHSGRTFDVQIVIIEHKSII
                                                                        SKERYDQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEY
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TFKDFPQMGRFTLRDEGKTIAIGKVLKL 494
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ORGANISM: Candida albicans
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Best Local Similarity 70.3
Matches 194; Conservative
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US-09-248-796A-19828
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US-09-248-796A-19828
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; ORGANISM: EF-lalpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 TGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGYN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 IKTDVVFMPVSGYSGANLKDHVDPK-ECPWY-----TGPTLLEYLDTMNHVDR 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 E---ALPGDNVGFNVKNVSVKDVRRGNVAGDSKNDPPMEAAGFTAQVIILNHPGQISAGY 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 22.3%; Score 801.5; DB 1; Length 462; Best Local Similarity 38.3%; Pred. No. 9e-62; Matches 169; Conservative 90; Mismatches 157; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                           1: FROM 1 TO 462
          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YPQLGRFTLRDQGTTIAIGKI 680
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cleveland Jr., Dan
REGISTRATION NUMBER: 3270
TELECOMUNICATION INFORMATION:
TELEPHONE: (816) 474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                      Uetsuki,
J. Biol. Chem.
264
                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                               PAGES: 5791-5798
                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL:
VOLUME: 2
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERNCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
FILE REPERSONCE: 2000-04-14
FILING DATE: 2000-10-20
FRIOR PELING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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APPLICANT: Miller, Sven
APPLICANT: Dalbage, Henrik
TITLE OF INVENTION: No. 6255185el Yeast Promoters Suitable For E:
TITLE OF INVENTION: No. 6255185el Yeast Promoters Suitable For E:
TITLE OF INVENTION: No. 6255185el Yeast Promoters Suitable For E:
TITLE REPERBNCE: 4791.204-US
CURRENT APPLICATION NUMBER: US/09/174,768
CURRENT FILING DATE: 1998-10-19
EARLIER APPLICATION NUMBER: 0589/96
EARLIER APPLICATION NUMBER: 0589/96
EARLIER APPLICATION NUMBER: 0589/96
EARLIER APPLICATION NUMBER: 0589/96
SARLIER APPLICATION NUMBER: 0589/96
SOFTWARE: FastSEQ for Windows Version 3.0
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LGRFAVRDMRQTVAVG-VIKSVE 441
Sequence 4, Application US/09174768; Patent No. 6265185; GENERAL INFORMATION:
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Matches 170;
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOJ307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-1/4
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PELING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTHWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 9571
LENGTH: 469
                                                                                                                                                                                                                                                           258 KDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNK 317
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                                                                                                                                                                                      Length 469;
                                                                                                                                                                                      22.2%; Score 797.5; DB 4; Length 38.5%; Pred. No. 2.1e-61; Live 88; Mismatches 158; Indels
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION VUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 9570
LERGTH: 469
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Patent No. 6812339
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                                                                                                                     TYPE: PRT
ORGANISM: Human
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; ORGANISM: Human
US-09-949-016-9571
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US-09-949-016-9570
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US-09-949-016-9571
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Length 469;
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22.2%; Score 797.5; DB 4; ilarity 38.5%; Pred. No. 2.1e-61; Conservative 88; Mismatches 158;
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US-09-309-572-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        660 YPQLGRFTLRDQGTTIAIGKI 680
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; Sequence 10, Application US/09309572
Patent No. 6440730
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 EERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYE 377
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                                                                                                  485 HINAPFMLPI--AAKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNI--YNETEN 540
                                                                                                                  EVDMAMCGEQVKLRIKGVEEEDISPGFVLTSPKN-PIKSVTKFVAQIAIVELKSIIAAGF 599
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                                                                                                                                                                                                                                                           125 AGISKNGQTREHALLAYTLGVKQLIVGVNKMDSTEPPYSQKRYEEIVKEVSTYIKKIGYN 184
                               ---TGPTLLEYLDTMNHVDR 484
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Von Laer, Meike-Dorothee

TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
FILE REFERENCE: 35-195

CURRENT PAPLICATION NUMBER: US/09/18,096

CURRENT PILING DATE: 2000-11-22

PRIOR FILING DATE: 1998-11-26

PRIOR FILING DATE: 1998-11-26

PRIOR FILING DATE: 1999-11-25

PRIOR FILING DATE: 1999-05-11

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 10

SEQ ID NO 10
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US-09-718-096-10
                                 438 IKTDVVFMPVSGYSGANLKDHVDPK-ECPWY----
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Patent No. 6589763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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US-09-718-096-10
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        600 GCVMHVHTAIEEVHIVKLIAKLERGTRIKSKKAPAFAKKGMKVIAVLETEAPVCVETYOD

        Db
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        QY
        660 YPQLGRFTLRPQGTTIAIGKI 680

        BD
        418 YPPLGRRPAVRDMRQTVAVGVI 438
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Search completed: July 1, 2005, 18:39:39 Job time : 58.3582 secs

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Sequence 17486, A
Sequence 1774, Ap
Sequence 17479, A
Sequence 17477, A
Sequence 2730, A
Sequence 2730, A
Sequence 3108, Ap
Sequence 8108, Ap
                                                                                                                                                                                                                                                           (without alignments)
1467.128 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-732-923-17486
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Listing first 45 summaries

    protein search, using sw model

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Maximum DB
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Sequence 18903, Sequence 210113, Sequence 17528, A Sequence 17110, Sequence 17126, A Sequence 17799, A Sequence 17799, A Sequence 17450, A Sequence 17450, A Sequence 17451, A Sequence 17451, A Sequence 17621, A Sequence 17652, A Sequence 17652, A Sequence 17652, A Sequence 17651, A
                                                                                                                          Sequence 40, Appl
Sequence 17097, A
Sequence 210116,
                                                       Sequence 231, App
Sequence 44453, A
Sequence 40, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 YQQYNPDAGYQQQYNPQGGYQ-QYNPQGGYQQQFNPQGGRGNYKNFNYNNNLQGYQAGFQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 PQSQGMSLNDFQKQQ---KQAAPKPKKTLKLVSSSGIKLANATKKVGTKPAESDKKEEEK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 QQSQGMTLDDFHKQKQTSQSAPPKQKKSLKLVSSSGIKLANATK----KPKEDEKKEEEP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGY-QAYNAQAQPAGGYYQNYQGYSGYQQGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Publication No. US20050108791A1

Publication No. US20050108791A1

GERERAL INFORMATION:

APPLICANT: Edgetton, Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

TITLE PERERENES: 38-15(52796)C

CURRENT FILING DATE: 2003-12-10

FRIOR APPLICATION NUMBER: 10/310,154

PRIOR PILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 1478
5 US-10-108-260A-3174
4 US-10-146-473-46
5 US-10-428-173-46
1 US-09-976-165-40
4 US-10-342-276-40
4 US-10-342-276-40
7 US-10-728-923-117097
5 US-10-428-99-210116
6 US-10-428-99-210116
6 US-10-428-99-210116
7 US-10-428-99-210113
7 US-10-732-923-17528
7 US-10-732-923-17528
7 US-10-732-923-17729
7 US-10-732-923-17728
7 US-10-732-923-17728
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; ORGANISM: Zygosaccharomyces rouxii
US-10-732-923-17478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 512; Conservative
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     Query Match
Best Local
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Sequence 7274, Application US/10032585

Publication No. US200301805331

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Bussey
ITILE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
CURRENT FILING DATE: 2001-12-20
SOFTWARE: Patentin version 3.1
SEQ ID NO 2274
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                                                                                                                                        HVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTNKEERNDGKTIE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNR 627
--EEPVKKEEKPVQTEEKTE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDQQNTQDQLSGAMANASLNGDQSKQQQQQQQQQNYYNPNAAQSFVPQGGYQQFQ
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                                                                                                                                                                                                           VGKAYFETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTR
                                                                                                                                                                                                                               EHALLAKTOGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGYNIKTDVVFMPV
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                  EKSELPKVEDLKISESTHNTNNANVTSADALIKEQEEEVDDEVVNDMFGGKDHVSLIFMG
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 ESDK-----KEEEKSAETKEPTKEPTKV-
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Best Local Similarity
Marches 471; Conserv
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                                       KKEEKKAEPKEQESKKEEP-KREGTPRPAAAKDEKKEDLPKLEKLKIKE---EQAAANAS 210
                                                                                                                                                                                                                                               ---GFQPQSQGMSLNDFQKQ--QKQAA---PKPKKTLKLVSSSGIKLANATKKVGT-KPA 166
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                                                                                                                                                                                                                                                                                                  NWSKERYDQCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLL 473
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                   SAETK - - EPTKEPTKVEEPVKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVT 233
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                                                                                                         GADSLIKEQEEEVDEGVVNDMFGGKDHMSIIFMGHVDAGKSTWGGNILYMTGSVDKRTVE
                                                                                                                                                                            SNQGNNQQNYQQYSQ-NGNQQQGNNRYQGYQAYNAQAQPA-GGYYQNYQGYSGYQQGGYQ
                                                                                       SADALIKEQEEEVDDEVVNDMFGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIE
                                                                                                                                                                                                                               EMIGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTV
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| Publication No. US20050108791A1
| GENERAL INFORMATION:
| APPLICANT: Edgerton, Michael D
| TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
| FILE REFERENCE: 38-15(52796)C
| CURRENT FILING DATE: 2003-12-10
| PRIOR FILING DATE: 2003-12-04
| NUMBER OF SEQ ID NOS: 24149
| SEQ ID NO 17486
| LENGTH: 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 67.7%
Matches 485; Conservative
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, OKGANISM: Candida maltosa
US-10-732-923-17486
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-NSYNNRGGYNNYNNYN------QQDQQPVQNQGMSLADFQKQQNAQANLNKPKKTLK 156
                                                                                                                                                          MFGGKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVM 313
                                                                                                                                                                         MFGGKDHVSIIFMGHVDAGKSTMGGNILYLTGSVDKRTVDKYEREAKDAGRQGWYLSWVM 331
                                                                                                                                                                                                             DINKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARK 373
                                                                                                                                                                                                                            GEYETGFERGGOTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRA 433
                                                                                                                                                                                                                                                                             IGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMNHVDRHINAPFMLP 493
                                                                                                                                                                                                                                                                                                                                                                        JAAKMKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAMCGEQVKL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                      56 QQEQQFGQYGQQQNYNQ-GGYNNYNNR----GGYSNNRGGYNNSNRGGYSNYN---SYN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 QQYNPQGGYQQYNPQGGYQQQFNPQGGRGNYKNFNYNNN---LQGYQAGF-----QPQSQ 122
                                                                   RIKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFSCVMHVHTAIEEVH
                                                                                                       BEKT----EEKSELP----KVEDLKISESTHN--TNNANVTSADALIKEQEEEVDDEVVND
 QQQFNPQGGRGNYKNFNYNNNLQGYQAGFQP-QSQGMSLNDFQKQQKQAA--PKPKKTLK
                                                    LVSSSGIKLANATKKVGTKPAESDKKEEEKSAETKEPTKEPTKVE---EPVKKEEKPVQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15(57796)
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 17107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-10-732-923-17107
Sequence 17107, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         691 TiAIGKITKV 700
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US-10-732-923-17107
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                           --- AESDKKEEEKSAETKEPTKVEEPVKKE
                                                               EKPVOTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKEQEEEVDDEVVNDMFG
                                                                                                                  GKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIEKYEREAKDAGRQGWYLSWVMDTN
                                                                                                                                                                                                                      ETGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLRAIGY
                                                                                                                                                                                                                                                                            437 NIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMNHVDRHINAPFMLPIAA
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Publication No. US20050108791A1

Publication No. US20050108791A1

APPLICANT: Edgerton. Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-15(52796)C

CURRENT FALICATION NUMBER: 10/10/732,923

CURRENT FILING DATE: 2003-12-10

FRIOR APPLICATION NUMBER: 10/310,154

PRIOR FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 24149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2283.5; DB 17; Lengtl
Pred. No. 9.6e-140;
); Mismatches 116; Indels
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64.0%; Prec
tive 70; N
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            NATKKVGT -- KP-
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IGKITKL 720
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US-10-732-923-17479
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US-10-732-923-17479
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22730
LENGTH: 690
                                                                                                                                                                                                                                                                                                                                                        NWSKERYDOCVSNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLL 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMIGGASQADVGVLVISARKGEYETGFERGGTREHALLAKTQGVNKMVVVVNKMDDPTV 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYLDTMNHVDRHINAPFMLPIAAKWKDLGTIVEGKIESGHIKKGQSTLLMPNKTAVEIQN 533
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QGGYQGNNRGGYSGRGRGGYRG-GYQGGYNNQYGNQGGYQG-GYQGGYDNQYGNQGGYQG 139
                                                                                     140 GY-----DNQYGYDQPEEPQEKTLTLEEYQKQKQEALNKLKKPKVGGALKIGGDKPKAG 193
                                                                                                                                                                                                                                                                               ADALIKEQEEEVDDEVVNDMFG-GKDHVSLIFMGHVDAGKSTMGGNLLYLTGSVDKRTIE 293
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                                                NYKNFNYNNNLQGYQAGFQPQSQGMSLNDFQKQQKQAAPKFKK-
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LOCATION: (1)..(690)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                 271 AAAAAALKKEVSQAKKESNVTNADALVKEQEEQIDASIVNDMFGGKDHMSIIFMGHVDAG 330
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                                                                      G-----MSINDFQKQQKQAA----PKPKKTLKL-VSSSGIKLANATKKVGTKPAES 168
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                                                                                                                  152 DOQOETGSGOMSLEDYÓKÓÓKESLNKLATKÞÝKKVLKLALASSTVKAPIVTKKKEEEÞVAQ 211
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                                                                                                                                                                   DKKEEEKSAE---TKEPTKEPTKVEE------PVKKEEKPVQTEEKTEEKS--EL
                                                                                                                                                                                                                                                                PKVEDLKISESTHNTNNANVTSADALIKEQEEEVDDEVVNDMFGGKDHVSLIFMGHVDAG
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TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15/52796/C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR PILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 17477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 742;
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51.2%; Pred. No. 2.6e-113;
ive 97; Mismatches 165;
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Publication No. US20050108791A1
GENERAL INFORMATION:
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US-10-732-923-17477
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Matches 384; Conservative
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                                                                                                                                                                                                                           GKPVSLSIGGGGAPK---AAPSLSIEKEASSKSSPKPAAPTPKPADAPAAKSEAASAPVS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVVVVNNKMD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIQNIYNETENEVDMAMCGEQVKLRIKGVEEEDISPGFVLTSPKRPIKSVTKFVAQIAIV 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELKSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKPPAFAKKGMKVIAVLETE 649
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                                                                                               86
                                                                                                                                                                                                                                                                                 RGNYKNFNYNNNLQGYQA-----GFQPQSQGMSLNDFQKQQKQAAPKPKKTLKLVS
                                                                                                                                                                                                                                                            TEEKTEEKSELPKVEDLK-------AD
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                                                                 QAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFNPQGG
                                                                                               QQQPFDPY-----GQQQGGYPQYG-----QYGQQQGYPQYGQYGYPQQ----
                                 88;
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   Length
                                 Indels
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 ; Score 1658; DB 15;
; Pred. No. 4.2e-99;
97; Mismatches 176;
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DB 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17101, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
FIGHERAL INFORMATION:
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMP
FILE REFERENCE: 38-15(52796)
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: 2003-12-04
NUMBER OF SEQ ID NOS: 24149
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 46.18;
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                                 Conservative
                  Similarity
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US-10-732-923-17101
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                  Best Local Sim
Matches 335;
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PUBLICACTION NO. US20040014955A1
GENERAL INFORMATION:
APPLICANT: Exception Alexey M.
APPLICANT: Exception Carlos
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCCCCUS NEOFORMANS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 10182-011-999
CURRENT APPLICATION NUMBER: US/10/320,797
CURRENT PILING DATE: 2002-12-16
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 3361
SEQ ID NO 3284
LENGTH: 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644
                                                                                                                                                                                                                                               AA--PAAQSKTETPAPKVTSESTKKETAAPPP---QETP--TKSADAELAKTPSAPAAAL
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                                                                                                                           74 GFVPVNNIAGGYPYAQYTGQG-------QNSNSPHPTKSYQQYYQ-KPTGNT
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                                                                   Gaps
                                                                 57;
                                   Length 690;
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                                                               Indels
                                   DB 15;
                               Query Match 46.7%; Score 1679.5; DB 15; Best Local Similarity 51.4%; Pred. No. 1.6e-100; Matches 332; Conservative 109; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3284
 US-10-369-493-22730
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Sequence 3108, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
                                                             ; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8108
          NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin version 3.1
SEQ ID NO 8108
LENGTH: 716
PRIOR FILING DATE: 2001-08-31
                                                                                                             Query Match
Best Local Similarity
Matches 332; Conserv
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Sequence 8108, Application US/10128714

Publication No. US20030119013A1

GENERAL INFORMATION:

APPLICANT: Jiang, Bo

APPLICANT: Tishkoff, Daniel

APPLICANT: Tishkoff, Daniel

APPLICANT: Lemieux, Sebastien M

TITLE OF INVENTION: Methods of Use

FILE REFERENCE: 10182-018-99

CURRENT FILING DATE: 2001-04-23

PRIOR PILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-06-05

PRIOR PILING DATE: 2001-06-05

PRIOR PILING DATE: 2001-06-05

PRIOR PILING DATE: 2001-07-09

PRIOR PILING DATE: 2001-07-09

PRIOR PILING DATE: 2001-07-09

PRIOR PILING DATE: 2001-07-09

PRIOR PILING DATE: 2001-07-09
             14;
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                                                                                                                                                                                                                                                                                               DAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGQTREHALLAKTQGVNKMVV 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAQIAIVELKSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRKSKKPPAFAKKGMKV 642
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                                      -GYQQQFNPQGGRGNYK--NFNYNN----N
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BEFRPRNMY--YGPQDCTMNCDANNMPYGHFMGYNQRYDDR----KYEPCNRDYSRQGMN
                                                                                                                                           DKKEEEKSAETKEPTKEPTKVEEPVKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTN
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             Gaps
             80;
ed. No. 4.2e-97;
Mismatches 117; Indels
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  Pred.
11 Similarity 48.4%; Pro 310; Conservative 134;
                                      QQYNPQGGYQQYNPQG---
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                                                                                                                                                                                                                                                           NDFQKQQKQAAPKPKKT-----LKLVSSSGIKLANATK--KVGT-KPAESDKKEEBKSA 177
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                                           186; Indels
  DB 14;
43.3%; Score 1557.5; DB llarity 46.6%; Pred. No. 1.4e-92 Conservative 99; Mismatches 18
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91 AAPPPP-----AGGAANNHGAGSGAGGRAAPVESSQEEQSLCEGSNSAVSMELSEPIVE 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGEYETGFERGGQTREHALLAKTQGVNKMVVVVNKMDDPTVNWSKERYDQCVSNVSNFLR 432
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                                                                                                                                          GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION:
NO. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3174
                                                                                                                                                                                                                                                                                                                                                                                                                                          38.0%; Score 1364.5; DB 15; Lengt
49.2%; Pred. No. 4e-80;
ative 96; Mismatches 169; Indels
          FASKGQTIIARLEVISSAGAVCVERFEDYNQMGRFTLRDQ 698
                                                                                                          Sequence 3174, Application US/10108260A Publication No. US20040005560A1
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Sequence 46, Application US/10146473

PUDIICATION NO. US20030108888A1

GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew
APPLICANT: Gout, Ivan
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Best Local Simi
Matches 271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.3%; Score 1519.5; DB 14; Lengt!
46.3%; Pred. No. 4e-90;
ive 98; Mismatches 183; Indels
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TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2001-04-27
PRIOR PLICATION NUMBER: US 60/285,697
PRIOR PLING DATE: 2001-04-27
PRIOR PLING DATE: 2001-06-05
PRIOR PLING DATE: 2001-06-05
PRIOR PLING DATE: 2001-06-05
PRIOR PLING DATE: 2001-06-09
PRIOR PLING DATE: 2001-06-09
PRIOR PLING DATE: 2001-06-09
PRIOR PLING DATE: 2001-08-31
PRIOR PLING DATE: 2001-08-31
SOFTWARE: PATCHIN NOWBER: US 60/316,362
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 3108
                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Aspergillus fumigatus US-10-128-714-3108
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Best Local Similarity 46.3*
Matches 324; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 425 SNVSNFLRAIGYNIKTDVVFMPVSGYSGANLKDHVDPKECPWYTGPTLLEYLDTMNHVDR 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   545 AMCGEQVKLRIKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFSCVMH 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHTAIEEVHIVKLLHKLEKGTNRKSKKPPAFAKKGMKVIAVLETEAPVÇVETYQDYPQLG 664
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Eveleigh, Deepa
APPLICANT: Bigwood, Douglas
TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF
FILE REFERENCE: 5152
CURRENT APPLICATION NUMBER: US/10/788,792
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US 60/450,655
PRIOR FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                      DB 14; Length 499;
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                                                                                                                                                                                                                                                                                                 139; Indels
                                                                                                                                                                                                                                                                  37.7%; Score 1354.5; DB 352.5%; Pred. No. 1.3e-79; tive 89; Mismatches 139
APPLICANT: Stockert, Elisabeth
APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Breast Cancer Antigens
FILE REFERENCE: L00464/70130(JRV)
CURRENT APPLICATION NUMBER: US/10/146,473
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US 60/291,150
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-15
SOFTWARE: PatentIn version 3.0
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 231, Application US/10788792
Publication No. US20040191819A1
GENERAL INFORMATION:
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                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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US-10-788-792-231
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Sequence 44453, Application US/10425114

Publication No. US2004003488A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Soreen, Steven E
APPLICANT: Soreen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 AVLVISARKGEFETGFEKGGGTREHAMLAKTAGVKHLIVLINKMDDFTVNWSNERYEECK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 KVEEP-VKKEEKPVQTEEKTEEKSELPKVEDLKISESTHNTNNANVTSADALIKEQEEEV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 SVDGPIRLPIVDKYKDMGTVVLGKLESGSICKGQQLVWMPNKHNVEVLGILSD-DVETDT 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGWYLSWVMDTNKEERNDGKTIEVGKAYFETEKRRYTILDAPGHKMYVSEMIGGASQADV 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545 AMCGEQVKLRIKGVEEEDISPGFVLTSPKNPIKSVTKFVAQIAIVELKSIIAAGFSCVMH 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                        Length 499;
                                                                                                                                                                                                                                                                                                                                                         1.3e-79:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: 700963269_FLI.pep
US-10-425-114-44453
                                                                                                                                                                                                                                                                                                                                                                                             37.7%; Score 1354.5; 52.5%; Pred. No. 1.3e
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 52.5% Matches 262; Conservative
                                                                                                                                              LENGTH: 499
TYPE: PRT ORGANISM: Homo sapiens
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ORGANISM: Glycine max
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                                                                                                                        152 IKLANATKKVGTKPAESDKKEE-EKSAETKEPTKEPTKVBEPVKKEEKPVQTEEKTEEKS 210
                                                                                 ELPKVEDLKISESTHNTNNANVTSADALIKEQEEEVDDEVVNDMFGGKDHVSLIFMGHVD 270
                                                                                              AYPETEKRRYTILDAPGHKMYVSEMIGGASQADVGVLVISARKGEYETGFERGGOTREHA 390
                                                                                                                                                                             391 LLAKTQCVNKMVVVVNKADDPTVNWSKERYDQCVSNVSNFLRAIGYNIKTDVVFMPVSGY 450
                                                                                                                                                                                                                     240 QLAKTLGVSKLLVVVNKMDEPTVQMSKERYDEIESKMVPFLKQSGYNVKKDVLFLPISGL 299
                                                                                                                                                                                                                                                                                            511 SGHIKKGQSTLLMPNKTAVEIQNIYNETENEVDMAMCGEQVKLRIKGVEEDISPGFVLT 570
                                                                                                                                                                                                                                                                                                       571 SPKNPIKSVTKFVAQIAIVEL--KSIIAAGFSCVMHVHTAIEEVHIVKLLHKLEKGTNRK 628
                                                                                                                                                                                                                                                                                                                                                 Query Match 37.2%; Score 1338.5; DB 15; Length 533; Best Local Similarity 49.4%; Pred. No. 1.6e-78; Matches 263; Conservative. 96; Mismatches 130; Indels 43; Gaps
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